GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: November 29, 2004, 08:42:07 ; Search time 227 Seconds
(without alignments)
8623.403 Million cell updates/sec

Title: US-09-989-920-100
Perfect score: 2754
Sequence: 1 gccagaagcagcctcagctt.....aaaaataaaaagatgcggcc 2754

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1747.6	63.5	1853	3	US-09-232-160-3	Sequence 3, Appli
	2	52	1.9	7218	1	US-08-232-463-14	Sequence 14, Appl
	3	49	1.8	6330	3	US-09-880-427-2	Sequence 2, Appli
	4	49	1.8	6330	3	US-09-306-538B-2	Sequence 2, Appli
	5	49	1.8	19806	4	US-09-740-028A-3	Sequence 3, Appli
	6	49	1.8	19806	4	US-10-118-037-3	Sequence 3, Appli
	7	47	1.7	265	4	US-09-513-999C-27278	Sequence 27278, A
c	8	42.6	1.5	640681	4	US-09-790-988-1	Sequence 1, Appli
	9	41.6	1.5	210	4	US-09-248-796A-12137	Sequence 12137, A
c	10	41.4	1.5	329	4	US-09-513-999C-10733	Sequence 10733, A
c	11	40.8	1.5	318	4	US-09-513-999C-11322	Sequence 11322, A
	12	40.8	1.5	398	4	US-09-513-999C-23077	Sequence 23077, A
	13	40.4	1.5	1141	4	US-09-806-708B-22	Sequence 22, Appl
	14	40.4	1.5	640681	4	US-09-790-988-1	Sequence 1, Appli
c	15	39.6	1.4	1107	4	US-09-248-796A-8906	Sequence 8906, Ap
c	16	39.4	1.4	588	3	US-09-328-111-321	Sequence 321, App
	17	39.4	1.4	5852	1	US-07-867-106-2	Sequence 2, Appli
	18	39	1.4	303	4	US-09-601-198-179	Sequence 179, App
c	19	38.8	1.4	9636	1	US-08-323-170B-1	Sequence 1, Appli
c	20	38.8	1.4	9636	3	US-08-954-441-1	Sequence 1, Appli
c	21	38.4	1.4	2422	1	US-07-867-106-5	Sequence 5, Appli
c	22	38.4	1.4	5852	1	US-07-867-106-2	Sequence 2, Appli
c	23	38.4	1.4	54945	4	US-09-967-669-10	Sequence 10, Appl
c	24	38.2	1.4	1099	4	US-09-270-767-11371	Sequence 11371, A
c	25	38.2	1.4	3009	4	US-09-248-796A-6806	Sequence 6806, Ap
c	26	38.2	1.4	3454	4	US-09-270-767-11909	Sequence 11909, A
c	27	38.2	1.4	5185	3	US-08-971-395-5	Sequence 5, Appli
c	28	38.2	1.4	8561	3	US-09-112-450-3	Sequence 3, Appli
c	29	38.2	1.4	8561	4	US-09-419-291A-3	Sequence 3, Appli
	30	38.2	1.4	98844	4	US-09-791-211-10	Sequence 10, Appl
c	31	38	1.4	2007	2	US-08-743-637B-169	Sequence 169, App
c	32	38	1.4	2007	3	US-08-526-840B-169	Sequence 169, App
c	33	38	1.4	2028	3	US-09-134-001C-1710	Sequence 1710, Ap
c	34	37.8	1.4	4140	3	US-08-894-731-2	Sequence 2, Appli
c	35	37.8	1.4	8920	2	US-08-446-855A-1	Sequence 1, Appli
c	36	37.8	1.4	8920	3	US-09-150-741-1	Sequence 1, Appli
c	37	37.8	1.4	1664976	4	US-08-916-421B-1	Sequence 1, Appli
c	38	37.8	1.4	1664976	4	US-09-692-570-1	Sequence 1, Appli
c	39	37.4	1.4	2663	1	US-08-136-743B-3	Sequence 3, Appli
c	40	37.4	1.4	6040	4	US-10-204-708-70	Sequence 70, Appl
	41	37.4	1.4	74962	4	US-09-685-853A-3	Sequence 3, Appli
c	42	37.2	1.4	942	4	US-09-270-767-3767	Sequence 3767, Ap
c	43	37.2	1.4	942	4	US-09-270-767-19049	Sequence 19049, A
	44	37.2	1.4	1928	4	US-09-674-826B-5	Sequence 5, Appli
c	45	36.8	1.3	80246	3	US-09-078-294-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-232-160-3
; Sequence 3, Application US/09232160
; Patent No. 6368794
; GENERAL INFORMATION:
; APPLICANT: Steve Daniel
; APPLICANT: James Gilmore
; APPLICANT: Susan G. Stuart
; APPLICANT: Laura Stuve
; TITLE OF INVENTION: DETECTION OF ALTERED EXPRESSION OF GENES REGULATING CELL
; TITLE OF INVENTION: PROLIFERATION
; FILE REFERENCE: PA-0003 US
; CURRENT APPLICATION NUMBER: US/09/232,160
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PERL Program
; SEQ ID NO 3
; LENGTH: 1853
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 1283330
US-09-232-160-3

Query Match 63.5%; Score 1747.6; DB 3; Length 1853;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1750; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy       994 TGTTTTCTCCCCCATCACAAAAAAAAAAAATTCTTATTTTTAGTAGACATGTATTTACCAA 1053
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Db         1 TGTTTTCTCCCCCATCACAAAAAAAAAAAATTCTTATTTTTAGTAGACATGTATTTACCAA 60

Qy      1054 AAATATGTACTCAATTATTGTATTTTGGATTTTATCAATTTAAAAATTGTGGAAATTTGT 1113
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 AAATATGTACTCAATTATTGTATTTTGGATTTTATCAATTTAAAAATTGTGGAAATTTGT 120

Qy      1114 TTGCTCTTACGCCAACATAATATTGATTTTGCCTCTTGGCTCTGAAAGCCCAAAATATTT 1173
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Db       121 TTGCTCTTACGCCAACATAATATTGATTTTGCCTCTTGGCTCTGAAAGCCCAAAATATTT 180

Qy      1174 ACCGTCTAGCCCGTTACAGAAAAAGTCTGCTGACTACTGAGCCAGACCTCCATTACCTCC 1233
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 ACCGTCTAGCCCGTTACAGAAAAAGTCTGCTGACTACTGAGCCAGACCTCCATTACCTCC 240

Qy      1234 ATCCCTGTTGGATTATTTAAAGAAAGCCTCAGACAGTAAGGGCTTTTTTAAAAGAATAAA 1293
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Db       241 ATCCCTGTTGGATTATTTAAAGAAAGCCTCAGACAGTAAGGGCTTTTTTAAAAGAATAAA 300

Qy      1294 ATGACTTGGTTTGCGCTTGGAAGCAGGGGAAGCATTCAGATGAGCGGTTTCTGCATTAAC 1353
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Db        301 ATGACTTGGTTTGCGCTTGGAAGCAGGGGAAGCATTCAGATGAGCGGTTTCTGCATTAAC 360
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Db        421 TGCTTCAGCTGGCTCCTGCAGAGTCCACCCCGCCTCGTGGTGGGAATGCAGAGCCCTTTG 480
Qy       1474 CTTTCCTTCTTGCCGCCTGCTTCCTGTTCCTGGGGACCCGCTGGGCCTTTGGTCTGCATC 1533
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Qy       1534 CCCTGGCCAGGTCCCTCAGGGTTGATGCGTGGAGAAGGACTTTGAGCAGTGGTGGGCAGC 1593
Db        541 CCCTGGCCAGGTCCCTCAGGGTTGATGCGTGGAGAAGGACTTTGAGCAGTGGTGGGCAGC 600
Qy       1594 AGTGGCCTCCTGGCCAGCTCACACTCTTGTCCTGGGAGGGGCAGCCTGATCTCACCTCCA 1653
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Qy       1654 CCTAGTACCTTGGGGACTGAGGACCTTTTGGCTTCTCTGGAGCCTGCAAGCCTCTTCCCA 1713
Db        661 CCTAGTACCTTGGGGACTGAGGACCTTTTGGCTTCTCTGGAGCCTGCAAGCCTCTTCCCA 720
Qy       1714 TGTGTCCAGCTGCTCTTCCTGCTACAAAGGGGACTGCTCACAGTGGCCTCAGCTTGGTGG 1773
Db        721 TGTGTCCAGCTGCTCTTCCTGCTACAAAGGGGACTGCTCACAGTGGCCTCAGCTTGGTGG 780
Qy       1774 TTTTGAGGGGCCGCCCCCCGGCCCTCCATAAGGGTATCCTGGGCCTGAGAATTCTGCATC 1833
Db        781 TTTTGAGGGGCCGCCCCCCGGCCCTCCATAAGGGTATCCTGGGCCTGAGAATTCTGCATC 840
Qy       1834 TGCCATTGGAGGATGGACAGCCTCAAATGGAAGGAGTCCCACGGGAGATGGGTCCGAGGT 1893
Db        841 TGCCATTGGAGGATGGACAGCCTCAAATGGAAGGAGTCCCACGGGAGATGGGTCCGAGGT 900
Qy       1894 CCGGCTGTGGCCATCCAGCCCCCTGTGGCTTGTCCAGCCTCTGTGCACCCCTGGTGTCTT 1953
Db        901 CCGGCTGTGGCCATCCAGCCCCCTGTGGCTTGTCCAGCCTCTGTGCACCCCTGGTGTCTT 960
Qy       1954 CACTCCAGGGGCAGACAGCAGCCACTGCAGTTCCTTTCTTCGTGAGTAACAGTAGTGATA 2013
Db        961 CACTCCAGGGGCAGACAGCAGCCACTGCAGTTCCTTTCTTCGTGAGTAACAGTAGTGATA 1020
Qy       2014 GCAGCTGGGGCTAACAGGCTAGGCTTTGTGTTCTGCGCATTTGGTCAGCTTCTCACTCGA 2073
Db       1021 GCAGCTGGGGCTAACAGGCTAGGCTTTGTGTTCTGCGCATTTGGTCAGCTTCTCACTCGA 1080
Qy       2074 TCCTCCCTAAAGCAATGGGGAGGCCCCCACTAGCCCAGTTTTCAGGAAGTCAACTGGGAG 2133
Db       1081 TCCTCCCTAAAGCAATGGGGAGGCCCCCACTAGCCCAGTTTTCAGGAAGTCAACTGGGAG 1140
Qy       2134 GTTAGATGGGGGCCAGGGTCCCACAGCTACTGATGGCCCGAGCCAGGTTGAGCTTCCTGG 2193
Db       1141 GTTAGATGGGGGCCAGGGTCCCACAGCTACTGATGGCCCGAGCCAGGTTGAGCTTCCTGG 1200
Qy       2194 TGTCCAGTCCGGATCCCACTTGCAGATCTCATGCTCTCAGATAGGTGGGACAAGTTCTTT 2253
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Qy       2254 TGTCACAGTGCTGGCTCTGTCCTGAGGCCTCATTGCTGGCTGGGTGTGCTCTGCTGGGAA 2313
Db       1261 TGTCACAGTGCTGGCTCTGTCCTGAGGCCTCATTGCTGGCTGGGTGTGCTCTGCTGGGAA 1320
Qy       2314 AAGCTTTGCGGGGCTTGCTTGGTTAACCACAGAAGAGAAGGGGACTGTTTGGGGTGCCTC 2373
Db       1321 AAGCTTTGCGGGGCTTGCTTGGTTAACCACAGAAGAGAAGGGGACTGTTTGGGGTGCCTC 1380
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Qy       2434 TTAAAATGATTTCTTTCTAAAGATGTAACCTCCACACCTTTCTCCAGATTGGGTGACTCT 2493
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Qy       2494 TTTCTAAAGGTGGTGGGAGTATCTGTCGGGGTGGTGTGGCCCTTGGATGGGTCAGGTGGG 2553
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Qy       2554 TGTGAGAGGTCCTGGGGAGGTGGGCGTTGAGCTCAAAGTTGTCCTACTGCCATGTTTTTG 2613
Db       1561 TGTGAGAGGTCCTGGGGAGGTGGGCGTTGAGCTCAAAGTTGTCCTACTGCCATGTTTTTG 1620
Qy       2614 TACCTGAAATAAAGCATATTTTGCACTTGTTACTGTACCATAGTGCGGACGAGAAGTCTG 2673
Db       1621 TACCTGAAATAAAGCATATTTTGCACTTGTTACTGTACCATAGTGCGGACGAGAAGTCTG 1680
Qy       2674 TATGTGGGATCTGTGCTTGGGTTAGAATGCAAATAAAACTCACATTTGTAAGAAAAAAAA 2733
Db       1681 TATGTGGGATCTGTGCTTGGGTTAGAATGCAAATAAAACTCACATTTGTAAGACAAAAAA 1740
Qy       2734 AAAAAATAAAAAGA 2747
Db       1741 AAAAACAAAAGAGA 1754
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RESULT 2
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-F1s

US-08-232-463-14

Query Match 1.9%; Score 52; DB 1; Length 7218;
Best Local Similarity 12.2%; Pred. No. 0.00018;
Matches 61; Conservative 213; Mismatches 228; Indels 0; Gaps 0;

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Qy       1276 CTTTTTTAAAAGAATAAAATGACTTGGTTTGCGCTTGGAAGCAGGGGAAGCATTCAGATG 1335
Db       1005 CGTTTGCCATACGCTCACAGAATTAATTCCGAGCTTGGCTGCAGGTCGAGGGAGCTTGCG 1064

Qy       1336 AGCGGTTTCTGCATTAACCCTGCCTATCACGCATCTCGTGTCCTGTGTGGCTGGCGAGCC 1395
Db       1065 ATYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1124

Qy       1396 CCCCTTGGAAGGTTCTGGTGCTTCAGCTGGCTCCTGCAGAGTCCACCCCGCCTCGTGGTG 1455
Db       1125 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1184

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Db       1185 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1244

Qy       1516 GGGCCTTTGGTCTGCATCCCCTGGCCAGGTCCCTCAGGGTTGATGCGTGGAGAAGGACTT 1575
Db       1245 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1304

Qy       1576 TGAGCAGTGGTGGGCAGCAGTGGCCTCCTGGCCAGCTCACACTCTTGTCCTGGGAGGGGC 1635
Db       1305 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1364

Qy       1636 AGCCTGATCTCACCTCCACCTAGTACCTTGGGGACTGAGGACCTTTTGGCTTCTCTGGAG 1695
Db       1365 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1424

Qy       1696 CCTGCAAGCCTCTTCCCATGTGTCCAGCTGCTCTTCCTGCTACAAAGGGGACTGCTCACA 1755
Db       1425 YYYYYYYYYYGTACCAAATTCTTCTATCTCTTTAACTACTTGCATAGATAGGTAATTACA 1484

Qy       1756 GTGGCCTCAGCTTGGTGGTTTT 1777
Db       1485 GTGATGCCTACATGCCGTTTTT 1506
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RESULT 3
US-09-880-427-2
; Sequence 2, Application US/09880427
; Patent No. 6358728
; GENERAL INFORMATION:
; APPLICANT: Simon, Andras
; APPLICANT: Eriksson, Ulf
; APPLICANT: Dryja, Thaddeus P.
; APPLICANT: Berson, Eliot
; APPLICANT: Yamamoto, Hioyuji
; TITLE OF INVENTION: Mutations in Nucleic Acid Molecules Encoding 11-Cis Retinol
; TITLE OF INVENTION: Dehydrogenase, The Mutated Proteins, and Uses Thereof
; FILE REFERENCE: LUD 5601
; CURRENT APPLICATION NUMBER: US/09/880,427
; CURRENT FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 09/306,538
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 2
; LENGTH: 6330
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 5357, 5448
; OTHER INFORMATION: nucleotide not determined
US-09-880-427-2

Query Match 1.8%; Score 49; DB 3; Length 6330;
Best Local Similarity 56.5%; Pred. No. 0.0013;
Matches 91; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

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Qy       1061 TACTCAATTATTGTATTTTGGATTTTATCAATTTAAAAATTGTGGAAATTTGTTTGCTCT 1120
Db       4714 TACAAGCTGATAATGGTTTTTTTTATTTTTAAATGGTTACATTGTAAACTGTTATATAAG 4773

Qy       1121 TACGCCAACATAATATTGATTTTGCCTCTTGGCTCTGAAAGCCCAAAATATTTACCGTCT 1180
Db       4774 TACCTGATAATATCATTAATTTTGTTTCTTGGCCTGCCATGCTTAAAATATTAACTCTCT 4833

Qy       1181 AGCCCGTTACAGAAAAAGTCTGCTGACTACTGAGCCAGACC 1221
Db       4834 GGCCCTTTAAGAAAAAAACGTGCTGACCCCTGCTCTAGATC 4874
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RESULT 4
US-09-306-538B-2
; Sequence 2, Application US/09306538B
; Patent No. 6372463
; GENERAL INFORMATION:
; APPLICANT: Simon, Andras
; APPLICANT: Eriksson, Ulf
; APPLICANT: Dryja, Thaddeus P.
; APPLICANT: Berson, Eliot
; APPLICANT: Yamamoto, Hioyuji
; TITLE OF INVENTION: Mutations in Nucleic Acid Molecules Encoding 11-Cis Retinol
; TITLE OF INVENTION: Dehydrogenase, The Mutated Proteins, and Uses Thereof
; FILE REFERENCE: LUD 5601
; CURRENT APPLICATION NUMBER: US/09/306,538B
; CURRENT FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 2
; LENGTH: 6330
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 5357, 5448
; OTHER INFORMATION: nucleotide not determined
US-09-306-538B-2

Query Match 1.8%; Score 49; DB 3; Length 6330;
Best Local Similarity 56.5%; Pred. No. 0.0013;
Matches 91; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

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Qy       1061 TACTCAATTATTGTATTTTGGATTTTATCAATTTAAAAATTGTGGAAATTTGTTTGCTCT 1120
Db       4714 TACAAGCTGATAATGGTTTTTTTTATTTTTAAATGGTTACATTGTAAACTGTTATATAAG 4773

Qy       1121 TACGCCAACATAATATTGATTTTGCCTCTTGGCTCTGAAAGCCCAAAATATTTACCGTCT 1180
Db       4774 TACCTGATAATATCATTAATTTTGTTTCTTGGCCTGCCATGCTTAAAATATTAACTCTCT 4833

Qy       1181 AGCCCGTTACAGAAAAAGTCTGCTGACTACTGAGCCAGACC 1221
Db       4834 GGCCCTTTAAGAAAAAAACGTGCTGACCCCTGCTCTAGATC 4874
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RESULT 5
US-09-740-028A-3
; Sequence 3, Application US/09740028A
; Patent No. 6410289
; GENERAL INFORMATION:
; APPLICANT: GONG, Fangcheng et al
; TITLE OF INVENTION: ISOLATED HUMAN DEHYDROGENASES, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING THESE HUMAN DEHYDROGENASES, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001054
; CURRENT APPLICATION NUMBER: US/09/740,028A
; CURRENT FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3

LENGTH: 19806
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(19806)
OTHER INFORMATION: n = A,T,C or G
US-09-740-028A-3

Query Match 1.8%; Score 49; DB 4; Length 19806;
Best Local Similarity 56.5%; Pred. No. 0.0031;
Matches 91; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

Qy 1061 TACTCAATTATTGTATTTTGGATTTTATCAATTTAAAAATTGTGGAAATTTGTTTGCTCT 1120
Db 16677 TACAAGCTGATAATGGTTTTTTTTATTTTTAAATGGTTACATTGTAAACTGTTATATAAG 16736

Qy 1121 TACGCCAACATAATATTGATTTTGCCTCTTGGCTCTGAAAGCCCAAAATATTTACCGTCT 1180
Db 16737 TACCTGATAATATCATTAATTTTGTTTCTTGGCCTGCCATGCTTAAAATATTAACTCTCT 16796

Qy 1181 AGCCCGTTACAGAAAAAGTCTGCTGACTACTGAGCCAGACC 1221
Db 16797 GGCCCTTTAAGAAAAAAACGTGCTGACCCCTGCTCTAGATC 16837

RESULT 6
US-10-118-037-3
Sequence 3, Application US/10118037
Patent No. 6797499
GENERAL INFORMATION:
APPLICANT: GONG, Pangcheng et al.
TITLE OF INVENTION: ISOLATED HUMAN DEHYDROGENASES, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING THESE HUMAN DEHYDROGENASES, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001054DIV
CURRENT APPLICATION NUMBER: US/10/118,037
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 09/740,028
PRIOR FILING DATE: 2000-12-20
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 19806
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(19806)
OTHER INFORMATION: n = A,T,C or G
US-10-118-037-3

Query Match 1.8%; Score 49; DB 4; Length 19806;
Best Local Similarity 56.5%; Pred. No. 0.0031;
Matches 91; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

Qy 1061 TACTCAATTATTGTATTTTGGATTTTATCAATTTAAAAATTGTGGAAATTTGTTTGCTCT 1120
Db 16677 TACAAGCTGATAATGGTTTTTTTTATTTTTAAATGGTTACATTGTAAACTGTTATATAAG 16736

Qy 1121 TACGCCAACATAATATTGATTTTGCCTCTTGGCTCTGAAAGCCCAAAATATTTACCGTCT 1180
Db 16737 TACCTGATAATATCATTAATTTTGTTTCTTGGCCTGCCATGCTTAAAATATTAACTCTCT 16796

Qy 1181 AGCCCGTTACAGAAAAAGTCTGCTGACTACTGAGCCAGACC 1221
Db 16797 GGCCCTTTAAGAAAAAAACGTGCTGACCCCTGCTCTAGATC 16837

RESULT 7
US-09-513-999C-27278
Sequence 27278, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 27278
LENGTH: 265
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 63
OTHER INFORMATION: k=g or t
US-09-513-999C-27278

Query Match 1.7%; Score 47; DB 4; Length 265;
Best Local Similarity 62.2%; Pred. No. 0.0005;
Matches 74; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

Qy 1103 TGGAAATTTGTTTGCTCTTACGCCAACATAATATTGATTTTGCCTCTTGGCTCTGAAAGC 1162
Db 20 TGTAAACTGTTATATAAGTACCTGATAATATCATTAATTTTGTKTCTTGGCCTGCCATGC 79

Qy 1163 CCAAAATATTTACCGTCTAGCCCGTTACAGAAAAAGTCTGCTGACTACTGAGCCAGACC 1221
Db 80 TTAAAATATTAACTCTCTGGCCCTTTAAGAAAAAAACGTGCTGACCCCTGCTCTAGATC 138

RESULT 8
US-09-790-988-1/c
Sequence 1, Application US/09790988
Patent No. 6632935
GENERAL INFORMATION:
APPLICANT: SHIGENOBU, SHUJI
APPLICANT: WATANABE, HIDEMI
APPLICANT: HATTORI, MASAHIRA
APPLICANT: SAKAKI, YOSHIYUKI
TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
FILE REFERENCE: 081356/0159
CURRENT APPLICATION NUMBER: US/09/790,988
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: JP2000-107160
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 640681
TYPE: DNA
ORGANISM: Buchnera sp.
US-09-790-988-1

Query Match 1.5%; Score 42.6; DB 4; Length 640681;
Best Local Similarity 59.5%; Pred. No. 3.7;
Matches 72; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

Qy 1023 TTCTTATTTTTAGTAGACATGTATTTACCAAAAATATGTACTCAATTATTGTATTTTGGA 1082
Db 390713 TTTTTATTTTTTTTAATCATATTTTTTTCAAGAAAATGAATGTCATTATTTTTTATGGAA 390654

Qy 1083 TTTTATCAATTTAAAAATTGTGGAAATTTGTTTGCTCTTACGCCAACATAATATTGATTT 1142
Db 390653 ATTTTGTGTTTTATTAAATCTGTAATTTTTTCCCTGTCTATAAAAATATTAGTTTGATTT 390594

Qy 1143 T 1143

```
Db     390593 T 390593


RESULT 9
US-09-248-796A-12137
; Sequence 12137, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
;  APPLICANT: Keith Weinstock et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
;  TITLE OF INVENTION:  FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: 107196.132
;  CURRENT APPLICATION NUMBER: US/09/248,796A
;  CURRENT FILING DATE:  1999-02-12
;  PRIOR APPLICATION NUMBER: US 60/074,725
;  PRIOR FILING DATE: 1998-02-13
;  PRIOR APPLICATION NUMBER: US 60/096,409
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 12137
;   LENGTH: 210
;   TYPE: DNA
;   ORGANISM: Candida albicans
US-09-248-796A-12137

  Query Match             1.5%;  Score 41.6;  DB 4;  Length 210;
  Best Local Similarity   67.0%;  Pred. No. 0.018;
  Matches   59;  Conservative    0;  Mismatches   29;  Indels    0;  Gaps    0;

Qy       1011 CAAAAAAAAAAATTCTTATTTTTAGTAGACATGTATTTACCAAAAATATGTACTCAATTA 1070
              || ||||||| | ||  ||||||| |  |||||  ||||  |||||  |     ||||| ||
Db         32 CAGAAAAAAATAATCAAATTTTTAATCCACATGGTTTTAAGAAAAAGAAAATCTCAAATA 91

Qy       1071 TTGTATTTTGGATTTTATCAATTTAAAA 1098
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Db         92 TTGCATTTCTTCTTTCAACTAATAAACA 119


RESULT 10
US-09-513-999C-10733/c
; Sequence 10733, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Duclert, A.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
;  FILE REFERENCE: 59.US2.REG
;  CURRENT APPLICATION NUMBER: US/09/513,999C
;  CURRENT FILING DATE:  2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/122,487
;  PRIOR FILING DATE: 1999-02-26
;  NUMBER OF SEQ ID NOS: 36681
;  SOFTWARE: Patent.pm
; SEQ ID NO 10733
;   LENGTH: 329
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-513-999C-10733

  Query Match             1.5%;  Score 41.4;  DB 4;  Length 329;
  Best Local Similarity   62.6%;  Pred. No. 0.03;
  Matches   82;  Conservative    0;  Mismatches   46;  Indels    3;  Gaps    1;

Qy       1044 TATTTACCAAAAATATGTACTCAATTATTGTATTTTGGATTTTATCAATTTAAAAATTGT 1103
              | | |  || ||| |  |     |||| | ||||||| ||||||||||  ||  |  |||
Db        323 TGTATCACACAAAAAATTCAAGTATTAATATATTTTGAATTTTATCAATAAAATATATGT 264

Qy       1104 GGAAATTTG---TTTGCTCTTACGCCAACATAATATTGATTTTGCCTCTTGGCTCTGAAA 1160
              | |||||||    ||  |  | |     | | |   |  ||||||||| |||||||  |||
Db        263 GAAAATTTTTCATTCTCATTAAATATATAAAAGCCTCAATTTTGCCTTTTGGCTCACAAA 204

Qy       1161 GCCCAAAATAT 1171
              ||| ||| | |
Db        203 GCCTAAACTTT 193


RESULT 11
US-09-513-999C-11322/c
; Sequence 11322, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Duclert, A.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
;  FILE REFERENCE: 59.US2.REG
;  CURRENT APPLICATION NUMBER: US/09/513,999C
;  CURRENT FILING DATE:  2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/122,487
;  PRIOR FILING DATE: 1999-02-26
;  NUMBER OF SEQ ID NOS: 36681
;  SOFTWARE: Patent.pm
; SEQ ID NO 11322
;   LENGTH: 318
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 16
;   OTHER INFORMATION: r=a or g
US-09-513-999C-11322

  Query Match             1.5%;  Score 40.8;  DB 4;  Length 318;
  Best Local Similarity   52.3%;  Pred. No. 0.044;
  Matches   90;  Conservative    0;  Mismatches   82;  Indels    0;  Gaps    0;

Qy        750 AGTGGGAACCTGTCCTCATGCCCTTCGTCCTGAGGAGCCCTGAGGTGGGCAGCAGGGGCC 809
              | || ||| ||   |    ||    || | |  || | ||  |||  | |||  |||||
Db        201 ACTGAGAAGCTCGGCCGCAGCAAGGCGGCGTCGGGGGGCCGCAGGGCGCCAGTGGGGGCA 142

Qy        810 AGGGGAAGTTTTCAGGCCTTCATCAAAGAGAACAACATCCTCAGCTCCGCACCCCTCATC 869
              ||  | |  |||||  |  |  || |  | ||||  || |||||||  ||||| ||
Db        141 GAGGCTATTCCTCAGGACACCGGCAGATCCATCCTCATCTCCATCTCCGCCACCCTCCTC 82

Qy        870 CTGTATCAGCACTTACCGGTGTGTGACTGCCCTTGTCAGCTAGCATACGGTG 921
              ||  |  | | |      |      || |  |||||||  | | ||  | ||
Db         81 CTTCGTTGCCTCCCGGGCTTCCTCCTCTCCTGTTGTCAGTTGGGATCAGCTG 30


RESULT 12
US-09-513-999C-23077
; Sequence 23077, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Duclert, A.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
;  FILE REFERENCE: 59.US2.REG
;  CURRENT APPLICATION NUMBER: US/09/513,999C
;  CURRENT FILING DATE:  2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/122,487
;  PRIOR FILING DATE: 1999-02-26
;  NUMBER OF SEQ ID NOS: 36681
;  SOFTWARE: Patent.pm
; SEQ ID NO 23077
;   LENGTH: 398
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 144
```

; OTHER INFORMATION: n=a, g, c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 145
; OTHER INFORMATION: m=a or c
US-09-513-999C-23077

Query Match 1.5%; Score 40.8; DB 4; Length 398;
Best Local Similarity 63.0%; Pred. No. 0.052;
Matches 63; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

Qy 1131 TAATATTGATTTTGCCTCTTGGCTCTGAAAGCCCAAAATATTTACCGTCTAGCCCGTTAC 1190
Db 197 TAGTTATGACAGAACCTCTATGGCCACAAAGTTTAAAATATTTACTATCTTGCTATTTAC 256

Qy 1191 AGAAAAAGTCTGCTGACTACTGAGCCAGACCTCCATTACC 1230
Db 257 AGAAAATATTTGCTGACTTCTGCCCTACAGAAACATAAGC 296

RESULT 13
US-09-806-708B-22
Sequence 22, Application US/09806708B
Patent No. 6784342
GENERAL INFORMATION:
APPLICANT: The University of British Columbia
TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
FILE REFERENCE: 4810-58741
CURRENT APPLICATION NUMBER: US/09/806,708B
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 60/147,133
PRIOR FILING DATE: 1999-08-04
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn version 3.0
SEQ ID NO 22
LENGTH: 1141
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
NAME/KEY: promoter
LOCATION: (1)..(1141)
OTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. FAE1 promoters
US-09-806-708B-22

Query Match 1.5%; Score 40.4; DB 4; Length 1141;
Best Local Similarity 9.4%; Pred. No. 0.15;
Matches 35; Conservative 167; Mismatches 169; Indels 0; Gaps 0;

Qy 965 AGGGAATATTATCTTTGAACCCAATGAAGTGTTTTCTCCCCCATCACAAAAAAAAAAAATT 1024
Db 53 MSKSRKWTWARMYCKYRRWYNNKSRWWKGWYKKKWYBCANNTSBRYHARRWKDMKTAYBM 112

Qy 1025 CTTATTTTTAGTAGACATGTATTTACCAAAAATATGTACTCAATTATTGTATTTTGGATT 1084
Db 113 TMTNKWGKTGWRHRYWRWRAMBDTVDHHYVTAMNNAWTTMCMMDKDDKRTRWWWKKNNNA 172

Qy 1085 TTATCAATTTAAAAATTGTGGAAATTTGTTTGCTCTTACGCCAACATAATATTGATTTTG 1144
Db 173 TGWDDDTKYHMWNNNGCBTVTWMVRYKTDRDWSBKRMNYGMBWWKNWSYDVTYYWWVWDD 232

Qy 1145 CCTCTTGGCTCTGAAAGCCCAAAATATTTACCGTCTAGCCCGTTACAGAAAAAGTCTGCT 1204
Db 233 MCKRKVRRWVRTRGRMRNYMVAWBTAHRRRYNNGWTBAMAYRRWTMNNNNNNAKAMCKRA 292

Qy 1205 GACTACTGAGCCAGACCTCCATTACCTCCATCCCTGTTGGATTATTTAAAGAAAGCCTCA 1264
Db 293 KYWGWNRABVNSTCTTWKSKTTKVRTSCWANNCRAGDANKDHKWWKWSAAMGVYWNNNNN 352

Qy 1265 GACAGTAAGGGCTTTTTTAAAAGAATAAAATGACTTGGTTTGCGCTTGGAAGCAGGGGAA 1324
Db 353 NNWTYKKARHBARWDWVWHSAWKKWHANAAHYSRKKWTBYKRKTMVNNNNGTTMWKRMWA 412

Qy 1325 GCATTCAGATG 1335

Db 413 WYWKMDMDWBG 423

RESULT 14
US-09-790-988-1
; Sequence 1, Application US/09790988
; Patent No. 6632935
; GENERAL INFORMATION:
; APPLICANT: SHIGENOBU, SHUJI
; APPLICANT: WATANABE, HIDEMI
; APPLICANT: HATTORI, MASAHIRA
; APPLICANT: SAKAKI, YOSHIYUKI
; TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
; FILE REFERENCE: 081356/0159
; CURRENT APPLICATION NUMBER: US/09/790,988
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: JP2000-107160
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 640681
; TYPE: DNA
; ORGANISM: Buchnera sp.
US-09-790-988-1

Query Match 1.5%; Score 40.4; DB 4; Length 640681;
Best Local Similarity 53.9%; Pred. No. 17;
Matches 83; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

Qy 980 TGAACCCAATGAAGTGTTTTCTCCCCCATCACAAAAAAAAAAAATTCTTATTTTTAGTAGA 1039
Db 473336 TTAAAAAAATCAATATTATCTTTTTCAATTATATAATTCTATTTATTCAATAGAATTATA 473395

Qy 1040 CATGTATTTACCAAAAATATGTACTCAATTATTGTATTTTGGATTTTATCAATTTAAAAA 1099
Db 473396 TAAAAGTGTTCCTAAATTATGAAATAATTTTTAAAAATTAACATTTTAACAAATTAGAAA 473455

Qy 1100 TTGTGGAAATTTGTTTGCTCTTACGCCAACATAA 1133
Db 473456 TCAGTAAATTATGTTTGTTCTTTTGATGAAATAA 473489

RESULT 15
US-09-248-796A-8906/c
; Sequence 8906, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 8906
; LENGTH: 1107
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-8906

Query Match 1.4%; Score 39.6; DB 4; Length 1107;
Best Local Similarity 52.4%; Pred. No. 0.26;
Matches 87; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

Qy 975 ATCTTTGAACCCAATGAAGTGTTTTCTCCCCCATCACAAAAAAAAAAAATTCTTATTTTTA 1034
Db 218 ATTTCTGAATTTATATTACTGTTGTTTCTGTTATTATTATTATTATTATTATTATTA 159

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Qy       1035 GTAGACATGTATTTACCAAAAATATGTACTCAATTATTGTATTTTGGATTTTATCAATTT 1094
              ||    | |  ||  ||||| |   || |  ||||   |  | ||  |  |   |||||
Db        158 TTATTATTATTATTTGCAAAAGTCATTATTGTATTAGAATTCTGTGATTGATTATAATTT 99

Qy       1095 AAAAATTGTGGAAATTTGTTTGCTCTTACGCCAACATAATATTGAT 1140
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Db         98 TGTAATTGATGAGATTGATGTCTTTGTAATTGTTCATTATTTTTAT 53
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Job time : 236 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: November 29, 2004, 08:42:07 ; Search time 8386 Seconds
(without alignments)
11966.971 Million cell updates/sec

Title: US-09-989-920-100
Perfect score: 2754
Sequence: 1 gccagaagcagcctcagctt.....aaaaataaaaagatgcggcc 2754

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_est2:*
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5: gb_est4:*
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7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	2726.8	99.0	3408	3	BC020554	Homo sapi
	2	692	25.1	747	6	CD512690	CD512690 AGENCOURT
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c	4	655	23.8	685	5	BU684754	BU684754 UI-CF-EN1
	5	640	23.2	642	5	BQ953674	BQ953674 AGENCOURT
c	6	629.8	22.9	791	4	BI518071	BI518071 603041774
c	7	615	22.3	640	5	BQ045123	BQ045123 UI-CF-EN1
c	8	608	22.1	625	6	CB305549	CB305549 UI-CF-EN1
	9	604.2	21.9	611	6	CD723979	CD723979 cj28g08.y
c	10	563.4	20.5	577	1	AI928242	AI928242 wo95h01.x
	11	562.8	20.4	768	4	BM019092	BM019092 603647129
	12	560.2	20.3	577	5	BU678926	BU678926 UI-CF-DU1
c	13	546	19.8	547	2	AW271767	AW271767 xs18a11.x
c	14	532.4	19.3	535	2	AW173671	AW173671 xj10g08.x
c	15	526	19.1	538	2	AW195353	AW195353 xn37d01.x
c	16	520	18.9	525	6	CA944724	CA944724 UI-CF-FN0
c	17	513.8	18.7	518	8	BZ369653	BZ369653 UP_473-19
c	18	513.4	18.6	515	1	AI434765	AI434765 ti20b01.x
c	19	513.2	18.6	518	1	AI678967	AI678967 tu60b06.x
c	20	508	18.4	508	1	AI151375	AI151375 qc84a01.x
c	21	506	18.4	506	2	BE138747	BE138747 xw94d11.x
c	22	506	18.4	507	5	BQ012939	BQ012939 UI-1-BC1p
c	23	501	18.2	501	1	AI831850	AI831850 wi52f07.x
c	24	500.4	18.2	522	2	BF223573	BF223573 7q77g11.x
	25	481	17.5	493	5	BQ082334	BQ082334 K-EST0087
c	26	479.2	17.4	487	2	BF592110	BF592110 7o04g03.x
c	27	476.4	17.3	490	2	BF437146	BF437146 7p67a02.x
c	28	473	17.2	473	1	AI453406	AI453406 tj37h08.x
c	29	467.4	17.0	472	5	BX110666	BX110666 BX110666
c	30	465.4	16.9	467	1	AI421402	AI421402 tf25e12.x
c	31	456	16.6	468	1	AI347069	AI347069 qp60c01.x
c	32	454.4	16.5	456	2	AW874390	AW874390 hp99d01.x
c	33	447.2	16.2	485	2	BE857167	BE857167 7g21d12.x
c	34	447	16.2	449	1	AI245431	AI245431 qk29e02.x
c	35	445.2	16.2	454	1	AI733680	AI733680 ov13h01.x
c	36	445	16.2	445	1	AI241361	AI241361 qk17e10.x
c	37	443	16.1	443	1	AI189643	AI189643 qd18f08.x
c	38	441.2	16.0	446	2	AW772502	AW772502 hn76d05.x
	39	436.8	15.9	440	4	BM055156	BM055156 ie91b10.y
c	40	434.4	15.8	436	1	AI522077	AI522077 ti78d10.x
c	41	429	15.6	429	1	AI347815	AI347815 qp02g08.x
c	42	425	15.4	425	1	AI985135	AI985135 wr98b04.x
c	43	424.2	15.4	460	2	BE671688	BE671688 7b60e04.x
c	44	423.4	15.4	425	2	AW439823	AW439823 hb88d02.x
c	45	420	15.3	445	1	AI985235	AI985235 ws01a03.x

ALIGNMENTS

RESULT 1
BC020554
LOCUS BC020554 3408 bp mRNA linear HTC 04-MAR-2003
DEFINITION Homo sapiens, clone IMAGE:3049181, mRNA.
ACCESSION BC020554
VERSION BC020554.1 GI:18088242
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3408)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (03-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 20 Row: a Column: 5
This clone has the following problem: retained intron.
FEATURES Location/Qualifiers
source 1. .3408
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3049181"
/tissue_type="Placenta, choriocarcinoma"
/clone_lib="NIH_MGC_10"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
ORIGIN

Query Match 99.0%; Score 2726.8; DB 3; Length 3408;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2731; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```
Qy       1 GCCAGAAGCAGCCTCAGCTTGGCAAGGTGTGGAGATGACTGCTGTTCCCTTCGCATTTGG 60
Db     671 GCCAGAAGCAGCCTCAGCTTGGCAAGGTGTGGAGATGACTGCTGTTCCCTTCGCATTTGG 730

Qy      61 GGAAAACAGGCTCCCTCGGTAGCTCGATGATCCTCTTTTGATCTTGTGTGACCTCCTGGA 120
Db     731 GGAAAACAGGCTCCCTCGGTAGCTCGATGATCCTCTTTTGATCTTGTGTGACCTCCTGGA 790

Qy     121 GAGTGGATGACGCTGGTGGCCTTAGCTTTTCTAGACAGTGTAAATTGCACTGGGCGATGT 180
Db     791 GAGTGGATGAAGCTGGTGGCCTTAGCTTTTCTAGACAGTGTAAGTGGCACTGGGCGAGGC 850

Qy     181 CCCCAGAGCAGGGCAAGGTCTCTAGAGCGGGTCTCCCACATGACTGGCTTCACACAGGCA 240
Db     851 CCCCAGAGCAGGGCAAGGTCTCTAGAGCGGGTCTCCCACATGACTGGCTTCACACAGGCA 910

Qy     241 CTTCCGCTCGGGTTGCATGCTCTGTGTCATCTTACCGGTCCAGGGTTGCAGGTAGGAAAT 300
Db     911 CTTCCGCTCGGGTTGCATGCTCTGTGTCATCTTACCGGTCCAGGGTTGCAGGTAGGAAAT 970

Qy     301 GTTTGTACCCTCTTCTGATTGCCACCTCCTTCCCATCGCCCCTTAGGGACAGGGCTTGAG 360
Db     971 GTTTGTACCCTCTTCTGATTGCCACCTCCTTCCCATCGCCCCTTAGGGACAGGGCTTGAG 1030

Qy     361 GGCCAGTGAGGCGCTGGTCAGGCACCCCAGGCCTCCTTGGGACCTGCCCAGGGGCACCCT 420
Db    1031 GGCCAGTGAGGTGCTGGTCAGGCACCCCAGGCCTCCTTGGGACCTGCCCAGGGGCACCCT 1090

Qy     421 GAGAGCTCCTGAAACCCCCACTTAGCTTCCAGACCTTTCTGCAAAAGCTCCTCCTGGCTT 480
Db    1091 GAGAGCTCCTGAAACCCCCACTTAGCTTCCAGACCTTTCTGCAAAAGCTCCTCCTGGCTT 1150

Qy     481 TCCTCCCTCCCCCAATCTATGGGTCACAGCTAACAGATCTGAGGGCAACTGCTGTGCTAG 540
Db    1151 TCCTCCCTCCCCCAATCTATGGGTCACAGCTAACAGATCTGAGGGCAACTGCTGTGCTAG 1210

Qy     541 TGGCCAGGGCTGCACCTGCCATCCCCGGCTCTGCCACTTTAGGGCCTTCTAGAGGCAGTG 600
Db    1211 TGGCCAGGGCTGCACCTGCCATCCCCGGCTCTGCCACTTTAGGGCCTTCTAGAGGCAGTG 1270

Qy     601 TCCTTAGGAAGTAGCTCTGAGGCATGGGTTTTCTGCTCCTGTGCAGGGCAGCTGATGGGA 660
Db    1271 TCCTTAGGAAGTAGCTCTGAGGCATGGGTTTTCTGCTCCTGTGCAGGGCAGCTGATGGGA 1330

Qy     661 TAAGGTGGGGAAGGACGGTCAGTGCTTGGGCCCCAGCTGGCCAGCCTGGCGATGGGGAAA 720
Db    1331 TAAGGTGGGGAAGGACGGTCAGTGCTTGGGCCCCAGCTGGCCAGCCTGGCGATGGGGAAA 1390

Qy     721 CCAAACCATGTCCCCCAGCGAAGGGCCAGAGTGGGAACCTGTCCTCATGCCCTTCGTCCT 780
Db    1391 CCAAACCATGTCCCCCAGCGAAGGGCCAGAGTGGGAACCTGTCCTCATGCCCTTCGTCCT 1450

Qy     781 GAGGAGCCCTGAGGTGGGCAGCAGGGGCCAGGGGAAGTTTTCAGGCCTTCATCAAAGAGA 840
Db    1451 GAGGAGCCCTGAGGTGGGCAGCAGGGGCCAGGGGAAGTTTTCAGGCCTTCATCAAAGAGA 1510

Qy     841 ACAACATCCTCAGCTCCGCACCCCTCATCCTGTATCAGCACTTACCGGTGTGTGACTGCC 900
Db    1511 ACAACATCCTCAGCTCCGCACCCCTCATCCTGTATCAGCACTTACCGGTGTGTGACTGCC 1570

Qy     901 CTTGTCAGCTAGCATACGGTGGGCCCACCTGGCCCACTGGCTGTTTATGCCACTGATTTA 960
Db    1571 CTTGTCAGCTAGCATACGGTGGGCCCACCTGGCCCACTGGCTGTTTATGCCACTGATTTA 1630

Qy     961 TGATAGGGAATATTATCTTTGAACCCAATGAAGTGTTTTCTCCCCCATCACAAAAAAAAA 1020
Db    1631 TGATAGGGAATATTATCTTTGAACCCAATGAAGTGTTTTCTCCCCCATCACAAAAAAAAA 1690

Qy    1021 AATTCTTATTTTTAGTAGACATGTATTTACCAAAAATATGTACTCAATTATTGTATTTTG 1080
Db    1691 AATTCTTATTTTTAGTAGACATGTATTTACCAAAAATATGTACTCAATTATTGTATTTTG 1750

Qy    1081 GATTTTATCAATTTAAAAATTGTGGAAATTTGTTTGCTCTTACGCCAACATAATATTGAT 1140
Db    1751 GATTTTATCAATTTAAAAATTGTGGAAATTTGTTTGCTCTTACGCCAACATAATATTGAT 1810

Qy    1141 TTTGCCTCTTGGCTCTGAAAGCCCAAAATATTTACCGTCTAGCCCGTTACAGAAAAAGTC 1200
Db    1811 TTTGCCTCTTGGCTCTGAAAGCCCAAAATATTTACCGTCTAGCCCGTTACAGAAAAAGTC 1870

Qy    1201 TGCTGACTACTGAGCCAGACCTCCATTACCTCCATCCCTGTTGGATTATTTAAAGAAAGC 1260
Db    1871 TGCTGACTACTGAGCCAGACCTCCATTACCTCCATCCCTGTTGGATTATTTAAAGAAAGC 1930

Qy    1261 CTCAGACAGTAAGGGCTTTTTTAAAAGAATAAAATGACTTGGTTTGCGCTTGGAAGCAGG 1320
Db    1931 CTCAGACAGTAAGGGCTTTTTTAAAAGAATAAAATGACTTGGTTTGCGCTTGGAAGCAGG 1990

Qy    1321 GGAAGCATTCAGATGAGCGGTTTCTGCATTAACCCTGCCTATCACGCATCTCGTGTCCTG 1380
Db    1991 GGAAGCATTCAGATGAGCGGTTTCTGCATTAACCCTGCCTATCACGCATCTCGTGTCCTG 2050

Qy    1381 TGTGGCTGGCGAGCCCCCCTTGGAAGGTTCTGGTGCTTCAGCTGGCTCCTGCAGAGTCCA 1440
Db    2051 TGTGGCTGGCGAGCCCCCCTTGGAAGGTTCTGGTGCTTCAGCTGGCTCCTGCAGAGTCCA 2110

Qy    1441 CCCCGCCTCGTGGTGGGAATGCAGAGCCCTTTGCTTTCCTTCTTGCCGCCTGCTTCCTGT 1500
Db    2111 CCCCGCCTCGTGGTGGGAATGCAGAGCCCTTTGCTTTCCTTCTTGCCGCCTGCTTCCTGT 2170

Qy    1501 TCCTGGGGACCCGCTGGGCCTTTGGTCTGCATCCCCTGGCCAGGTCCCTCAGGGTTGATG 1560
Db    2171 TCCTGGGGACCCGCTGGGCCTTTGGTCTGCATCCCCTGGCCAGGTCCCTCAGGGTTGATG 2230

Qy    1561 CGTGGAGAAGGACTTTGAGCAGTGGTGGGCAGCAGTGGCCTCCTGGCCAGCTCACACTCT 1620
Db    2231 CGTGGAGAAGGACTTTGAGCAGTGGTGGGCAGCAGTGGCCTCCTGGCCAGCTCACACTCT 2290

Qy    1621 TGTCCTGGGAGGGGCAGCCTGATCTCACCTCCACCTAGTACCTTGGGGACTGAGGACCTT 1680
Db    2291 TGTCCTGGGAGGGGCAGCCTGATCTCACCTCCACCTAGTACCTTGGGGACTGAGGACCTT 2350

Qy    1681 TTGGCTTCTCTGGAGCCTGCAAGCCTCTTCCCATGTGTCCAGCTGCTCTTCCTGCTACAA 1740
Db    2351 TTGGCTTCTCTGGAGCCTGCAAGCCTCTTCCCATGTGTCCAGCTGCTCTTCCTGCTACAA 2410

Qy    1741 AGGGGACTGCTCACAGTGGCCTCAGCTTGGTGGTTTTGAGGGGCCGCCCCCCGGCCCTCC 1800
Db    2411 AGGGGACTGCTCACAGTGGCCTCAGCTTGGTGGTTTTGAGGGGCCGCCCCCCGGCCCTCC 2470

Qy    1801 ATAAGGGTATCCTGGGCCTGAGAATTCTGCATCTGCCATTGGAGGATGGACAGCCTCAAA 1860
Db    2471 ATAAGGGTATCCTGGGCCTGAGAATTCTGCATCTGCCATTGGAGGATGGACAGCCTCAAA 2530

Qy    1861 TGGAAGGAGTCCCACGGGAGATGGGTCCGAGGTCCGGCTGTGGCCATCCAGCCCCCTGTG 1920
Db    2531 TGGAAGGAGTCCCACGGGAGATGGGTCCGAGGTCCGGCTGTGGCCATCCAGCCCCCTGTG 2590

Qy    1921 GCTTGTCCAGCCTCTGTGCACCCCTGGTGTCTTCACTCCAGGGGCAGACAGCAGCCACTG 1980
Db    2591 GCTTGTCCAGCCTCTGTGCACCCCTGGTGTCTTCACTCCAGGGGCAGACAGCAGCCACTG 2650

Qy    1981 CAGTTCCTTTCTTCGTGAGTAACAGTAGTGATAGCAGCTGGGGCTAACAGGCTAGGCTTT 2040
Db    2651 CAGTTCCTTTCTTCGTGAGTAACAGTAGTGATAGCAGCTGGGGCTAACAGGCTAGGCTTT 2710

Qy    2041 GTGTTCTGCGCATTTGGTCAGCTTCTCACTCGATCCTCCCTAAAGCAATGGGGAGGCCCC 2100
Db    2711 GTGTTCTGCGCATTTGGTCAGCTTCTCACTCGATCCTCCCTAAAGCAATGGGGAGGCCCC 2770

Qy    2101 CACTAGCCCAGTTTTCAGGAAGTCAACTGGGAGGTTAGATGGGGGCCAGGGTCCCACAGC 2160
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Db       2771 CACTAGCCCAGTTTTCAGGAAGTCAACTGGGAGGTTAGATGGGGGCCAGGGTCCCACAGC 2830

Qy       2161 TACTGATGGCCCGAGCCAGGTTGAGCTTCCTGGTGTCCAGTCCGGATCCCACTTGCAGAT 2220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2831 TACTGATGGCCCGAGCCAGGTTGAGCTTCCTGGTGTCCAGTCCGGATCCCACTTGCAGAT 2890

Qy       2221 CTCATGCTCTCAGATAGGTGGGACAAGTTCTTTTGTCACAGTGCTGGCTCTGTCCTGAGG 2280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2891 CTCATGCTCTCAGATAGGTGGGACAAGTTCTTTTGTCACAGTGCTGGCTCTGTCCTGAGG 2950

Qy       2281 CCTCATTGCTGGCTGGGTGTGCTCTGCTGGGAAAAGCTTTGCGGGGCTTGCTTGGTTAAC 2340
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Db       2951 CCTCATTGCTGGCTGGGTGTGCTCTGCTGGGAAAAGCTTTGCGGGGCTTGCTTGGTTAAC 3010

Qy       2341 CACAGAAGAGAAGGGGACTGTTTGGGGTGCCTCTCTGCAGCCTCCCCGTGCTGGGTGGAA 2400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3011 CACAGAAGAGAAGGGGACTGTTTGGGGTGCCTCTCTGCAGCCTCCCCGTGCTGGGTGGAA 3070

Qy       2401 GCACGGTTACTGTGTTCTCTAATGTTCATGTATTTAAAATGATTTCTTTCTAAAGATGTA 2460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3071 GCACGGTTACTGTGTTCTCTAATGTTCATGTATTTAAAATGATTTCTTTCTAAAGATGTA 3130

Qy       2461 ACCTCCACACCTTTCTCCAGATTGGGTGACTCTTTTCTAAAGGTGGTGGGAGTATCTGTC 2520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3131 ACCTCCACACCTTTCTCCAGATTGGGTGACTCTTTTCTAAAGGTGGTGGGAGTATCTGTC 3190

Qy       2521 GGGGTGGTGTGGCCCTTGGATGGGTCAGGTGGGTGTGAGAGGTCCTGGGGAGGTGGGCGT 2580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3191 GGGGTGGTGTGGCCCTTGGATGGGTCAGGTGGGTGTGAGAGGTCCTGGGGAGGTGGGCGT 3250

Qy       2581 TGAGCTCAAAGTTGTCCTACTGCCATGTTTTTGTACCTGAAATAAAGCATATTTTGCACT 2640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3251 TGAGCTCAAAGTTGTCCTACTGCCATGTTTTTGTACCTGAAATAAAGCATATTTTGCACT 3310

Qy       2641 TGTTACTGTACCATAGTGCGGACGAGAAGTCTGTATGTGGGATCTGTGCTTGGGTTAGAA 2700
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3311 TGTTACTGTACCATAGTGCGGACGAGAAGTCTGTATGTGGGATCTGTGCTTGGGTTAGAA 3370

Qy       2701 TGCAAATAAAACTCACATTTGTAAGAAAAAAAAAAAAA 2738
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Db       3371 TGCAAATAAAACTCACATTTGTAAAAAAAAAAAAAAAA 3408
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RESULT 2
CD512690
LOCUS       CD512690                747 bp    mRNA    linear   EST 06-JUN-2003
DEFINITION  AGENCOURT_14360615 NIH_MGC_186 Homo sapiens cDNA clone
            IMAGE:30406456 5', mRNA sequence.
ACCESSION   CD512690
VERSION     CD512690.1  GI:31444408
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 747)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
             cDNA Library Preparation: CLONTECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: NDCM195  row: d  column: 17
            High quality sequence stop: 509.
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FEATURES             Location/Qualifiers
     source          1. .747
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:30406456"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_186"
                     /note="Organ: Pooled-Skin; Vector: pDNR-LIB; Site_1: SfiI
                     (ggccattatggcc); Site_2: SfiI (ggccgcctcggcc); Library is
                     oligo-dT primed and directionally cloned. cDNA was
                     prepared from a pooled samples of tissues from Skin,
                     meninges, duramatter, pia matter and choroid plexus.   5'
                     and 3' adaptors were used in cloning as follows: 5'
                     adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor
                     sequence: 5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3'
                     (where B = A, C, or G and N = A, C, G, or T). Average
                     insert size 1.47 kb (range 0.50-4.0 kb).  15/15 colonies
                     contained inserts by PCR. This library was enriched for
                     full-length clones and was constructed by Clontech
                     Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
                     Library"
ORIGIN
```

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  Query Match             25.1%;  Score 692;  DB 6;  Length 747;
  Best Local Similarity   98.5%;  Pred. No. 8.3e-171;
  Matches  709;  Conservative    0;  Mismatches   10;  Indels    1;  Gaps    1;

Qy       1842 GAGGATGGACAGCCTCAAATGGAAGGAGTCCCACGGGAGATGGGTCCGAGGTCCGGCTGT 1901
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGGATGGACAGCCTCAAATGGAAGGAGTCCCACGGGAGATGGGTCCGAGGTCCGGCTGT 60

Qy       1902 GGCCATCCAGCCCCCTGTGGCTTGTCCAGCCTCTGTGCACCCCTGGTGTCTTCACTCCAG 1961
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGCCATCCAGCCCCCTGTGGCTTGTCCAGCCTCTGTGCACCCCTGGTGTCTTCACTCCAG 120

Qy       1962 GGGCAGACAGCAGCCACTGCAGTTCCTTTCTTCGTGAGTAACAGTAGTGATAGCAGCTGG 2021
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGCAGACAGCAGCCACTGCAGTTCCTTTCTTCGTGAGTAACAGTAGTGATAGCAGCTGG 180

Qy       2022 GGCTAACAGGCTAGGCTTTGTGTTCTGCGCATTTGGTCAGCTTCTCACTCGATCCTCCCT 2081
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GGCTAACAGGCTAGGCTTTGTGTTCTGCGCATTTGGTCAGCTTCTCACTCGATCCTCCCT 240

Qy       2082 AAAGCAATGGGGAGGCCCCCACTAGCCCAGTTTTCAGGAAGTCAACTGGGAGGTTAGATG 2141
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAGCAATGGGGAGGCCCCCACTAGCCCAGTTTTCAGGAAGTCAACTGGGAGGTTAGATG 300

Qy       2142 GGGGCCAGGGTCCCACAGCTACTGATGGCCCGAGCCAGGTTGAGCTTCCTGGTGTCCAGT 2201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGGGCCAGGGTCCCACAGCTACTGATGGCCCGAGCCAGGTTGAGCTTCCTGGTGTCCAGT 360

Qy       2202 CCGGATCCCACTTGCAGATCTCATGCTCTCAGATAGGTGGGACAAGTTCTTTTGTCACAG 2261
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CCGGATCCCACTTGCAGATCTCATGCTCTCAGATAGGTGGGACAAGTTCTTTTGTCACAG 420

Qy       2262 TGCTGGCTCTGTCCTGAGGCCTCATTGCTGGCTGGGTGTGCTCTGCTGGGAAAAGCTTTG 2321
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGCTGGCTCTGTCCTGAGGCCTCATTGCTGGCTGGGTGTGCTCTGCTGGGAAAAGCTTTG 480

Qy       2322 CGGGGCTTGCTTGGTTAACCACAGAAGAGAAGGGGACTGTTTGGGGTGCCTCTCTGCAGC 2381
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CGGGGCTTGCTTGGTTAACCACAGAAGAGAAGGGGACTGTTTGGGGTGCCTCTCTGCAGC 540

Qy       2382 CTCCCCGTGCTGGGTGGAAGCACGGTTACTGTGTTCTCTAATGTTCATGTATTTAAAATG 2441
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTCCCCGTGCTGGGTGGAAGCACGGTTACTGTGTTCTCTAATGTTCATGTATTTAAAATG 600

Qy       2442 ATTTCTTTCTAAAGATGTAACCTCCACACCTTTCTCCAGATTGGGTGACTCTTTTCTAAA 2501
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ATTTCTTTCTAAAGATGTAACCTCCACACCTTTCTCCAGATTGGGTGACTCTTTTCTAAA 660

Qy       2502 GGTGGTGGGAGTATCTGTCGGGGTGGTGTGG-CCCTTGGATGGGTCAGGTGGGTGTGAGA 2560
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Db        661 GGGGGTGGGAGTATCTGTCGGGGTGGTGTGGCCCCTTGGATGGGTTCAAGTGGGGTGTGA 720


RESULT 3
CB242367/c
LOCUS       CB242367                766 bp    mRNA    linear   EST 12-FEB-2003
DEFINITION  UI-CF-FN0-age-m-22-0-UI.s1 UI-CF-FN0 Homo sapiens cDNA clone
            UI-CF-FN0-age-m-22-0-UI 3', mRNA sequence.
ACCESSION   CB242367
VERSION     CB242367.1  GI:28364011
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 766)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
   PUBMED   8889548
COMMENT     Contact: McCray, PB
            McCray Lab
            University of Iowa
            2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
            Tel: 319 356 4866
            Fax: 319 356 7171
            Email: paul-mccray@uiowa.edu
            Tissue Procurement: Dr. M. J. Welsh, University of Iowa
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com) or from Open Biosystems
            (www.openbiosystems.com).
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-CF-FN0-age-m-22-0-UI"
                     /tissue_type="Human Lung Epithelial cells"
                     /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                     /clone_lib="UI-CF-FN0"
                     /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     UI-CF-FN0 is a subtracted cDNA library derived from two
                     normalized Human lung epithelial cell libraries (EN1 and
                     DU1) The library was subtracted according to according to
                     Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                     1996. For additional information, contact:
                     bento-soares@uiowa.edu
                     TAG_TISSUE=Human Lung Epithelial Cell Lines untreated LPS
                     6hr to LPS 24h
                     TAG_LIB=UI-CF-FN0
                     TAG_SEQ=CTGCTCAGGT"
ORIGIN

  Query Match            24.7%;  Score 680.4;  DB 6;  Length 766;
  Best Local Similarity  97.6%;  Pred. No. 9.6e-168;
  Matches  723;  Conservative    0;  Mismatches   12;  Indels    6;  Gaps    3;

Qy       1999 GTAACAGTAGTGATAGCAGCTGGGGCTAACAGGCTAGGCTTTGTGTTCTGCGCATTTGGT 2058
             |||||||||||||||||||||||      |          |||||||||||||| | ||
Db        736 GTAACAGTAGTGATAGCAGCTGGG----CTAACAGCTAGCTTGTGTTCTGCGCATNT-GT 682

Qy       2059 CAGCTTCTCACTCGATCCTCCCTAAAGCAATGGGGAGGCCCCCACTAGCCCAGTTTTCAG 2118
             |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        681 CAGCTTCTCACTCGATCCTCCCTAAAGCAATGGGG-GGCCCCCACTAGCCCAGTTTTCAG 623

Qy       2119 GAAGTCAACTGGGAGGTTAGATGGGGGCCAGGGTCCCACAGCTACTGATGGCCCGAGCCA 2178
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        622 GAAGTCAACTGGGAGGTTAGATGGGGGCCAGGGTCCCACAGCTACTGATGGCCCGAGCCA 563

Qy       2179 GGTTGAGCTTCCTGGTGTCCAGTCCGGATCCCACTTGCAGATCTCATGCTCTCAGATAGG 2238
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        562 GGTTGAGCTTCCTGGTGTCCAGTCCGGATCCCACTTGCAGATCTCATGCTCTCAGATAGG 503

Qy       2239 TGGGACAAGTTCTTTTGTCACAGTGCTGGCTCTGTCCTGAGGCCTCATTGCTGGCTGGGT 2298
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        502 TGGGACAAGTTCTTTTGTCACAGTGCTGGCTCTGTCCTGAGGCCTCATTGCTGGCTGGGT 443

Qy       2299 GTGCTCTGCTGGGAAAAGCTTTGCGGGGCTTGCTTGGTTAACCACAGAAGAGAAGGGGAC 2358
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Db        442 GTGCTCTGCTGGGAAAAGCTTTGCGGGGCTTGCTTGGTTAACCACAGAAGAGAAGGGGAC 383

Qy       2359 TGTTTGGGGTGCCTCTCTGCAGCCTCCCCGTGCTGGGTGGAAGCACGGTTACTGTGTTCT 2418
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Db        382 TGTTTGGGGTGCCTCTCTGCAGCCTCCCCGTGCTGGGTGGAAGCACGGTTACTGTGTTCT 323

Qy       2419 CTAATGTTCATGTATTTAAAATGATTTCTTTCTAAAGATGTAACCTCCACACCTTTCTCC 2478
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        322 CTAATGTTCATGTATTTAAAATGATTTCTTTCTAAAGATGTAACCTCCACACCTTTCTCC 263

Qy       2479 AGATTGGGTGACTCTTTTCTAAAGGTGGTGGGAGTATCTGTCGGGGTGGTGTGGCCCTTG 2538
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        262 AGATTGGGTGACTCTTTTCTAAAGGTGGTGGGAGTATCTGTCGGGGTGGTGTGGCCCTTG 203

Qy       2539 GATGGGTCAGGTGGGTGTGAGAGGTCCTGGGGAGGTGGGCGTTGAGCTCAAAGTTGTCCT 2598
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Db        202 GATGGGTCAGGTGGGTGTGAGAGGTCCTGGGGAGGTGGGCGTTGAGCTCAAAGTTGTCCT 143

Qy       2599 ACTGCCATGTTTTTGTACCTGAAATAAAGCATATTTTGCACTTGTTACTGTACCATAGTG 2658
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Db        142 ACTGCCATGTTTTTGTACCTGAAATAAAGCATATTTTGCACTTGTTACTGTACCATAGTG 83

Qy       2659 CGGACGAGAAGTCTGTATGTGGGATCTGTGCTTGGGTTAGAATGCAAATAAAACTCACAT 2718
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          82 CGGACGAGAAGTCTGTATGTGGGATCTGTGCTTGGGTTAGAATGCAAATAAAACTCACAT 23

Qy       2719 TTGTAAGAAAAAAAAAAAAAA 2739
             |||||||||||||||||||||
Db          22 TTGTAAGAAAAAAAAAAAAAA 2


RESULT 4
BU684754/c
LOCUS       BU684754                685 bp    mRNA    linear   EST 07-OCT-2002
DEFINITION  UI-CF-EN1-acv-d-09-0-UI.s1 UI-CF-EN1 Homo sapiens cDNA clone
            UI-CF-EN1-acv-d-09-0-UI 3', mRNA sequence.
ACCESSION   BU684754
VERSION     BU684754.1  GI:23538028
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 685)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
   PUBMED   8889548
COMMENT     Contact: McCray, PB
            McCray Lab
            University of Iowa
            2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
            Tel: 319 356 4866
            Fax: 319 356 7171
            Email: paul-mccray@uiowa.edu
            Tissue Procurement: Dr. M. J. Welsh, University of Iowa
```

```
            cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
            cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: Researchers may obtain clones from Research
           Genetics (www.resgen.com) or from Open Biosystems
           (www.openbiosystems.com).
           Seq primer: M13 FORWARD
           POLYA=Yes.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
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                     /tissue_type="Primary Lung Cystic Fibrosis Epithelial
                     Cells"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                     /clone_lib="UI-CF-EN1"
                     /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     UI-CF-EN1 is a normalized cDNA library containing the
                     following tissue(s): Primary Lung Cystic Fibrosis
                     Epithelial Cells. The library was constructed according to
                     Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                     1996. First strand cDNA synthesis was primed with an
                     oligo-dT primer containing a Not I site.  Double stranded
                     cDNA was ligated to an EcoR I adaptor, digested with Not
                     I, and cloned directionally into pT7T3-Pac vector. The
                     oligonucleotide used to prime the synthesis of
                     first-strand cDNA contains a library tag sequence that is
                     located between the Not I site and the (dT)18 tail. The
                     sequence tag for this library is CTGCTCAGGT.
                     TAG_TISSUE=Human Lung Epithelial Cell Lines untreated LPS
                     6hr to LPS 24h
                     TAG_LIB=UI-CF-EN1
                     TAG_SEQ=CTGCTCAGGT"
ORIGIN

  Query Match             23.8%;  Score 655;  DB 5;  Length 685;
  Best Local Similarity   98.5%;  Pred. No. 4.7e-161;
  Matches  669;  Conservative    0;  Mismatches    9;  Indels    1;  Gaps    1;

Qy        345 AGGGACAGGGCTTGAGGGCCAGTGAGGCGCTGGTCAGGCACCCCAGGCCTCCTTGGGACC 404
              ||| |||||||||||||||||||||| |||||||||||||| |||||||||||| ||||
Db        685 AGGNACAGGGCTTGAGGGCCAGTGAGGTGCTGGTCAGGCACCNCAGGCCTCCTTGNGACC 626

Qy        405 TGCCCAGGGGCACCCTGAGAGCTCCTGAAACCCCCACTTAGCTTCCAGACCTTTCTGCAA 464
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 TGCCCAGGGGCACCCTGAGAGCTCCTGAAACCCCCACTTAGCTTCCAGACCTTTCTGCAA 566

Qy        465 AAGCTCCTCCTGGCTTTCCTCCCTCCCCCAATCTATGGGTCACAGCTAACAGATCTGAGG 524
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 AAGCTCCTCCTGGCTTTCCTCCCTCCCCCAATCTATGGGTCACAGCTAACAGATCTGAGG 506

Qy        525 GCAACTGCTGTGCTAGTGGCCAGGGCTGCACCTGCCATCCCCGGCTCTGCCACTTTAGGG 584
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        505 GCAACTGCTGTGCTAGTGGCCAGGGCTGCACCTGCCATCCCCGGCTCTGCCACTTTAGGG 446

Qy        585 CCTTCTAGAGGCAGTGTCCTTAGGAAGTAGCTCTGAGGCATGGGTTTTCTGCTCCTGTGC 644
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 CCTTCTAGAGGCAGTGTCCTTAGGAAGTAGCTCTGAGGCATGGGTTTTCTGCTCCTGTGC 386

Qy        645 AGGGCAGCTGATGGGATAAGGTGGGGAAGGACGGTCAGTGCTTGGGCCCCAGCTGGCCAG 704
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 AGGGCAGCTGATGGGATAAGGTGGGGAAGGACGGTCAGTGCTTGGGCCCCAGCTGGCCAG 326

Qy        705 CCTGGCGATGGGGAAACCAAACCATGTCCCCCAGCGAAGGGCCAGAGTGGGAACCTGTCC 764
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 CCTGGCGATGGGGAAACCAAACCATGTCCCCCAGCGAAGGGCCAGAGTGGGAACCTGTCC 266

Qy        765 TCATGCCCTTCGTCCTGAGGAGCCCTGAGGTGGGCAGCAGGGGCCAGGGGAAGTTTTCAG 824
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        265 TCATGCCCTTCGTCCTGAGGAGCCCTGAGGTGGGCAGCAGGGGCCAGGGGAAGTTTTCAG 206

Qy        825 GCCTTCATCAAAGAGAACAACATCCTCAGCTCCGCACCCCTCATCCTGTATCAGCACTTA 884
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 GCCTTCATCAAAGAGAACAACATCCTCAGCTCCGCACCCCTCATCCTGTATCAGCACTTA 146

Qy        885 CCGGTGTGTGACTGCCCTTGTCAGCTAGCATACGGTGGGCCCACCTGGCCCACTGGCTGT 944
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 CCGGTGTGTGACTGCCCTTGTCAGCTAGCATACGGTGGGCCCACCTGGCCCACTGGCTGT 86

Qy        945 TTATGCCACTGATTTATGATAGGGAATATTATCTTTGAACCCAA-TGAAGTGTTTTCTCC 1003
              |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db         85 TTATGCCACTGATTTATGATAGGGAATATTATCTTTGAACCCAAGTGAAGTGTTTTCTCC 26

Qy       1004 CCCATCACAAAAAAAAAAA 1022
              ||||     ||||||||||
Db         25 CCCANTCACAAAAAAAAAA 7


RESULT 5
BQ953674
LOCUS       BQ953674                642 bp    mRNA    linear   EST 21-AUG-2002
DEFINITION  AGENCOURT_8803100 Lupski_sciatic_nerve Homo sapiens cDNA clone
            IMAGE:6198871 5', mRNA sequence.
ACCESSION   BQ953674
VERSION     BQ953674.1  GI:22369152
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 642)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. James R. Lupski
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLAM13611  row: d  column: 08
           High quality sequence stop: 600.
FEATURES             Location/Qualifiers
     source          1. .642
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6198871"
                     /sex="male"
                     /tissue_type="sciatic nerve"
                     /dev_stage="adult, 70 yr"
                     /lab_host="DH10B"
                     /clone_lib="Lupski_sciatic_nerve"
                     /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
                     NotI; Site_2: SalI; cDNA made by oligo-dT priming.
                     Directionally cloned using the following adaptors:
                     5'-TCGACCCACGCGTCCG-3' and
                     5'-GACTAGTTCTAGATCGCGAGCGGCCGCCCT(15)-3'. Size selected >
                     1 kb for average insert length 1.87 kb. This is a primary
                     library, non-amplified. Library constructed by Life
                     Technologies and donated  by J. Lupski, M.D./Ph.D. (Baylor
                     College of Medicine) and is available through Life
                     Technologies."
ORIGIN

  Query Match             23.2%;  Score 640;  DB 5;  Length 642;
  Best Local Similarity   100.0%;  Pred. No. 4.2e-157;
  Matches  640;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy       2100 CCACTAGCCCAGTTTTCAGGAAGTCAACTGGGAGGTTAGATGGGGGCCAGGGTCCCACAG 2159
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCACTAGCCCAGTTTTCAGGAAGTCAACTGGGAGGTTAGATGGGGGCCAGGGTCCCACAG 60

Qy       2160 CTACTGATGGCCCGAGCCAGGTTGAGCTTCCTGGTGTCCAGTCCGGATCCCACTTGCAGA 2219
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTACTGATGGCCCGAGCCAGGTTGAGCTTCCTGGTGTCCAGTCCGGATCCCACTTGCAGA 120

Qy       2220 TCTCATGCTCTCAGATAGGTGGGACAAGTTCTTTTGTCACAGTGCTGGCTCTGTCCTGAG 2279
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCTCATGCTCTCAGATAGGTGGGACAAGTTCTTTTGTCACAGTGCTGGCTCTGTCCTGAG 180

Qy       2280 GCCTCATTGCTGGCTGGGTGTGCTCTGCTGGGAAAAGCTTTGCGGGGCTTGCTTGGTTAA 2339
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCTCATTGCTGGCTGGGTGTGCTCTGCTGGGAAAAGCTTTGCGGGGCTTGCTTGGTTAA 240

Qy       2340 CCACAGAAGAGAAGGGGACTGTTTGGGGTGCCTCTCTGCAGCCTCCCCGTGCTGGGTGGA 2399
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CCACAGAAGAGAAGGGGACTGTTTGGGGTGCCTCTCTGCAGCCTCCCCGTGCTGGGTGGA 300

Qy       2400 AGCACGGTTACTGTGTTCTCTAATGTTCATGTATTTAAAATGATTTCTTTCTAAAGATGT 2459
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AGCACGGTTACTGTGTTCTCTAATGTTCATGTATTTAAAATGATTTCTTTCTAAAGATGT 360

Qy       2460 AACCTCCACACCTTTCTCCAGATTGGGTGACTCTTTTCTAAAGGTGGTGGGAGTATCTGT 2519
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACCTCCACACCTTTCTCCAGATTGGGTGACTCTTTTCTAAAGGTGGTGGGAGTATCTGT 420

Qy       2520 CGGGGTGGTGTGGCCCTTGGATGGGTCAGGTGGGTGTGAGAGGTCCTGGGGAGGTGGGCG 2579
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CGGGGTGGTGTGGCCCTTGGATGGGTCAGGTGGGTGTGAGAGGTCCTGGGGAGGTGGGCG 480

Qy       2580 TTGAGCTCAAAGTTGTCCTACTGCCATGTTTTTGTACCTGAAATAAAGCATATTTTGCAC 2639
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTGAGCTCAAAGTTGTCCTACTGCCATGTTTTTGTACCTGAAATAAAGCATATTTTGCAC 540

Qy       2640 TTGTTACTGTACCATAGTGCGGACGAGAAGTCTGTATGTGGGATCTGTGCTTGGGTTAGA 2699
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTGTTACTGTACCATAGTGCGGACGAGAAGTCTGTATGTGGGATCTGTGCTTGGGTTAGA 600

Qy       2700 ATGCAAATAAAACTCACATTTGTAAGAAAAAAAAAAAAAA 2739
             ||||||||||||||||||||||||||||||||||||||||
Db        601 ATGCAAATAAAACTCACATTTGTAAGAAAAAAAAAAAAAA 640
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RESULT 6
BI518071/c
LOCUS BI518071 791 bp mRNA linear EST 29-AUG-2001
DEFINITION 603041774T1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5162851 3', mRNA sequence.
ACCESSION BI518071
VERSION BI518071.1 GI:15342863
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 791)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11404 row: d column: 20
High quality sequence start: 10
High quality sequence stop: 759.

FEATURES Location/Qualifiers
source 1. .791
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5162851"
/lab_host="DH10B"
/clone_lib="NIH_MGC_116"
/note="Organ: pooled colon, kidney, stomach; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library."
ORIGIN

Query Match 22.9%; Score 629.8; DB 4; Length 791;
Best Local Similarity 96.2%; Pred. No. 2.2e-154;
Matches 753; Conservative 0; Mismatches 17; Indels 13; Gaps 10;

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Qy       1882 TGGGTCCGAGGTCCGGCTGTGGCCAT--CCAGCCCCCTGTGGC-TTGTCCAGCCTCTGTG 1938
             ||| |||||||||||||||||||||||  |  ||||||||||| |||||||||||||||||
Db        791 TGGTTCCGAGGTCCGGCTGTGGCCATTCCAGGCCCCCTGTGGCATTGTCCAGCCTCTGTG 732

Qy       1939 CACCCCTGGTGTCTTCACT-CCAGGGGCAGACAGCAGCCACTGCAGTTCCTTTCTTCGTG 1997
             ||| |||||||||| |||||| |||||||||||||||||||||||| |||| ||||||||
Db        731 CACACCTGGTGTCTTCACTCCCAGGGGCAGACAGCAGCCACTGCAGCTCCTCTCTTCGTG 672

Qy       1998 AGTAACAGTAGTGATAGCAGCTGGGGCTAACAGGCTAGGCTTTGTGTTC-TGCGCATTTG 2056
             |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        671 AGTAACAGTAGTGATAGCAGCTGGGGCTAACAGGCTAGGCTTTGTGTTCATGCGCATTTG 612

Qy       2057 GTCAGCTTCTCACTCGATCCTCCCTAAAGCAATGGGGAGGCCCCCACTAGCCCAGTTTTC 2116
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        611 GTCAGCTTCTCACTCGATCCTCCCTAAAGCAATGGGGAGGCCCCCACTAGCCCAGTTTTC 552

Qy       2117 AGGAAGTCAACTGGGAGGTTAGATGGGGGCCAGGGTCCCACAGCTACTGATGGCCCGAGC 2176
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        551 AGGAAGTCAACTGGGAGGTTAGATGGGGGCCAGGGTCCCACAGCTACTGATGGCCCGAGC 492

Qy       2177 CAGGTTGAGCTTCCTGGTGTCCAGTCCGGATCCCACTTGCAGATCTCATGCTCTCAGATA 2236
             ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        491 CAGGTCGAGCTTCCTGGTGTCCAGTCCGGATCCCACTTGCAGATCTCATGCTCTCAGATA 432

Qy       2237 GGTGGGACAAGTTCTTTTGTCACAGTGCTGGCTCTGTCCTGAGGCCTCATTGCTGGCTGG 2296
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        431 GGTGGGACAAGTTCTTTTGTCACAGTGCTGGCTCTGTCCTGAGGCCTCATTGCTGGCTGG 372

Qy       2297 GTGTGCTCTGCTGGGAAAAGCTTTGCGGGGCTTGC-TTGGTTAACCACAGAAGAGAAGGG 2355
             |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db        371 GTGTGCTCTGCTGGGAAAAGCTTTGCGGGGCTTGCATTGGTTAACCACAGAAGAGAAGGG 312

Qy       2356 GACTGTTTGGGGTGCCTCTCTGCAGCCTCCCCGTGCTGGG-TGGAAGCACGGT-TACTGT 2413
             |||||||||||||||||||||||||||||||||||||||| |||||||||||| ||||||
Db        311 GACTGTTTGGGGTGCCTCTCTGCAGCCTCCCCGTGCTGGGCTGGAAGCACGGTCTACTGT 252

Qy       2414 GTTCTCTAA---TGTTCATGTATTTAAAATGATTTCTTTCTAAAGATGTAACCTCCACAC 2470
             ||||||| |   |   |    ||||||||||||||||||||||||||||||||||||||
Db        251 GTTCTCTCAATGTTCACTGTACTTTAAAATGATTTCTTTCTAAAGATGTAACCTCCACAC 192

Qy       2471 CTTTCTCCAGATTGGGTGACTCTTTTCTAAAGGTGGTGGGAGTATCTG-TCGGGGTGGTG 2529
             |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        191 CTTTCTCCAGATTGGGTGACTCTTTTCTAAAGGTGGTGGGAGTATCTGCTCGGGGTGGTG 132

Qy       2530 TGGCCCTTGGATGGGTCAGGTGGGTGTGAGAGGTCCT-GGGGAGGTGGGCGTTGAGCTCA 2588
             |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db        131 TGGCCCTTGGATGGGTCAGGTGGGTGTGAGAGGTCCTCGGGGAGGTGGGCGTTGAGCTCA 72
```

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Qy       2589 AAGTTGTCCTACTGCCATGTTTTTGTACCTGAAATAAAGCATATTTTGCACTTGTTACTG 2648
             ||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db         71 AAGTTGTCCTACTGCCATGTTTGTGTACCTGAAATAAAGCATATTTTGCACTTGTTACTG 12

Qy       2649 TAC 2651
             |||
Db         11 TAC 9


RESULT 7
BQ045123/c
LOCUS       BQ045123                640 bp    mRNA    linear   EST 21-FEB-2003
DEFINITION  UI-CF-EN1-ael-i-10-0-UI.s1 UI-CF-EN1 Homo sapiens cDNA clone
            UI-CF-EN1-ael-i-10-0-UI 3', mRNA sequence.
ACCESSION   BQ045123
VERSION     BQ045123.1  GI:19796176
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 640)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
   PUBMED   8889548
COMMENT     Contact: McCray, PB
            McCray Lab
            University of Iowa
            2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
            Tel: 319 356 4866
            Fax: 319 356 7171
            Email: paul-mccray@uiowa.edu
            Tissue Procurement: Dr. M. J. Welsh, University of Iowa
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com) or from Open Biosystems
            (www.openbiosystems.com).
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .640
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-CF-EN1-ael-i-10-0-UI"
                     /tissue_type="Primary Lung Cystic Fibrosis Epithelial
                     Cells"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                     /clone_lib="UI-CF-EN1"
                     /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     UI-CF-EN1 is a normalized cDNA library containing the
                     following tissue(s): Primary Lung Cystic Fibrosis
                     Epithelial Cells. The library was constructed according to
                     Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                     1996. First strand cDNA synthesis was primed with an
                     oligo-dT primer containing a Not I site.  Double stranded
                     cDNA was ligated to an EcoR I adaptor, digested with Not
                     I, and cloned directionally into pT7T3-Pac vector. The
                     oligonucleotide used to prime the synthesis of
                     first-strand cDNA contains a library tag sequence that is
                     located between the Not I site and the (dT)18 tail. The
                     sequence tag for this library is CTGCTCAGGT.
                     TAG_TISSUE=Human Lung Epithelial Cell Lines untreated LPS
                     6hr to LPS 24h
                     TAG_LIB=UI-CF-EN1
                     TAG_SEQ=CTGCTCAGGT"
ORIGIN

  Query Match             22.3%;  Score 615;  DB 5;  Length 640;
  Best Local Similarity   98.6%;  Pred. No. 1.6e-150;
  Matches  630;  Conservative    0;  Mismatches    7;  Indels    2;  Gaps    1;

Qy       2103 CTAGCCCAGTTTTCAGG--AAGTCAACTGGGAGGTTAGATGGGGGCCAGGGTCCCACAGC 2160
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Db        640 CTAGCCCAGTTNTCAGGGAAGTCAACNTGGGAGGTTAGATGGGGGCCAGGGTCCCACAGC 581

Qy       2161 TACTGATGGCCCGAGCCAGGTTGAGCTTCCTGGTGTCCAGTCCGGATCCCACTTGCAGAT 2220
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Db        580 TACTGATGGCCCGAGCCAGGTTGAGCTTCCTGGTGTCCAGTCCGGATCCCACTTGCAGAT 521

Qy       2221 CTCATGCTCTCAGATAGGTGGGACAAGTTCTTTTGTCACAGTGCTGGCTCTGTCCTGAGG 2280
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Db        520 CTCATGCTCTCAGATAGGTGGGACAAGTTCTTTTGTCACAGTGCTGGCTCTGTCCTGAGG 461

Qy       2281 CCTCATTGCTGGCTGGGTGTGCTCTGCTGGGAAAAGCTTTGCGGGGCTTGCTTGGTTAAC 2340
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Db        460 CCTCATTGCTGGCTGGGTGTGCTCTGCTGGGAAAAGCTTTGCGGGGCTTGCTTGGTTAAC 401

Qy       2341 CACAGAAGAGAAGGGGACTGTTTGGGGTGCCTCTCTGCAGCCTCCCCGTGCTGGGTGGAA 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        400 CACAGAAGAGAAGGGGACTGTTTGGGGTGCCTCTCTGCAGCCTCCCCGTGCTGGGTGGAA 341

Qy       2401 GCACGGTTACTGTGTTCTCTAATGTTCATGTATTTAAAATGATTTCTTTCTAAAGATGTA 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        340 GCACGGTTACTGTGTTCTCTAATGTTCATGTATTTAAAATGATTTCTTTCTAAAGATGTA 281

Qy       2461 ACCTCCACACCTTTCTCCAGATTGGGTGACTCTTTTCTAAAGGTGGTGGGAGTATCTGTC 2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        280 ACCTCCACACCTTTCTCCAGATTGGGTGACTCTTTTCTAAAGGTGGTGGGAGTATCTGTC 221

Qy       2521 GGGGTGGTGTGGCCCTTGGATGGGTCAGGTGGGTGTGAGAGGTCCTGGGGAGGTGGGCGT 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        220 GGGGTGGTGTGGCCCTTGGATGGGTCAGGTGGGTGTGAGAGGTCCTGGGGAGGTGGGCGT 161

Qy       2581 TGAGCTCAAAGTTGTCCTACTGCCATGTTTTTGTACCTGAAATAAAGCATATTTTGCACT 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        160 TGAGCTCAAAGTTGTCCTACTGCCATGTTTTTGTACCTGAAATAAAGCATATTTTGCACT 101

Qy       2641 TGTTACTGTACCATAGTGCGGACGAGAAGTCTGTATGTGGGATCTGTGCTTGGGTTAGAA 2700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        100 TGTTACTGTACCATAGTGCGGACGAGAAGTCTGTATGTGGGATCTGTGCTTGGGTTAGAA 41

Qy       2701 TGCAAATAAAACTCACATTTGTAAGAAAAAAAAAAAAAA 2739
             ||||||||||||||||||||||||||||||||||||||||
Db         40 TGCAAATAAAACTCACATTTGTAAGAAAAAAAAAAAAA 2


RESULT 8
CB305549/c
LOCUS       CB305549                625 bp    mRNA    linear   EST 04-MAR-2003
DEFINITION  UI-CF-EN1-aed-n-21-0-UI.s1 UI-CF-EN1 Homo sapiens cDNA clone
            UI-CF-EN1-aed-n-21-0-UI 3', mRNA sequence.
ACCESSION   CB305549
VERSION     CB305549.1  GI:28846060
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 625)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
   PUBMED   8889548
COMMENT     Contact: McCray, PB
            McCray Lab
            University of Iowa
```

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            2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
            Tel: 319 356 4866
            Fax: 319 356 7171
            Email: paul-mccray@uiowa.edu
            Tissue Procurement: Dr. M. J. Welsh, University of Iowa
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com) or from Open Biosystems
            (www.openbiosystems.com).
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES              Location/Qualifiers
     source           1. .625
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="UI-CF-EN1-aed-n-21-0-UI"
                      /tissue_type="Primary Lung Cystic Fibrosis Epithelial
                      Cells"
                      /dev_stage="Adult"
                      /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                      /clone_lib="UI-CF-EN1"
                      /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                      modified polylinker; Site_1: EcoR I; Site_2: Not I;
                      UI-CF-EN1 is a normalized cDNA library containing the
                      following tissue(s): Primary Lung Cystic Fibrosis
                      Epithelial Cells. The library was constructed according to
                      Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                      1996. First strand cDNA synthesis was primed with an
                      oligo-dT primer containing a Not I site.  Double stranded
                      cDNA was ligated to an EcoR I adaptor, digested with Not
                      I, and cloned directionally into pT7T3-Pac vector. The
                      oligonucleotide used to prime the synthesis of
                      first-strand cDNA contains a library tag sequence that is
                      located between the Not I site and the (dT)18 tail. The
                      sequence tag for this library is CTGCTCAGGT.
                      TAG_TISSUE=Human Lung Epithelial Cell Lines untreated LPS
                      6hr to LPS 24h
                      TAG_LIB=UI-CF-EN1
                      TAG_SEQ=CTGCTCAGGT"
ORIGIN

  Query Match             22.1%;  Score 608;  DB 6;  Length 625;
  Best Local Similarity   99.8%;  Pred. No. 1.1e-148;
  Matches  619;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy        404 CTGCCCAGGGGCACCCTGAGAGCTCCTGAAACCCCCACTTAGCTTCCAGACCTTTCTGCA 463
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 CTGCCCAGGGGCACCCTGAGAGCTCCTGAAACCCCCACTTAGCTTCCAGACCTTTCTGCA 566

Qy        464 AAAGCTCCTCCTGGCTTTCCTCCCTCCCCCAATCTATGGGTCACAGCTAACAGATCTGAG 523
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 AAAGCTCCTCCTGGCTTTCCTCCCTCCCCCAATCTATGGGTCACAGCTAACAGATCTGAG 506

Qy        524 GGCAACTGCTGTGCTAGTGGCCAGGGCTGCACCTGCCATCCCCGGCTCTGCCACTTTAGG 583
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        505 GGCAACTGCTGTGCTAGTGGCCAGGGCTGCACCTGCCATCCCCGGCTCTGCCACTTTAGG 446

Qy        584 GCCTTCTAGAGGCAGTGTCCTTAGGAAGTAGCTCTGAGGCATGGGTTTTCTGCTCCTGTG 643
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 GCCTTCTAGAGGCAGTGTCCTTAGGAAGTAGCTCTGAGGCATGGGTTTTCTGCTCCTGTG 386

Qy        644 CAGGGCAGCTGATGGGATAAGGTGGGGAAGGACGGTCAGTGCTTGGGCCCCAGCTGGCCA 703
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 CAGGGCAGCTGATGGGATAAGGTGGGGAAGGACGGTCAGTGCTTGGGCCCCAGCTGGCCA 326

Qy        704 GCCTGGCGATGGGGAAACCAAACCATGTCCCCCAGCGAAGGGCCAGAGTGGGAACCTGTC 763
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 GCCTGGCGATGGGGAAACCAAACCATGTCCCCCAGCGAAGGGCCAGAGTGGGAACCTGTC 266

Qy        764 CTCATGCCCTTCGTCCTGAGGAGCCCTGAGGTGGGCAGCAGGGGCCAGGGGAAGTTTTCA 823
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 CTCATGCCCTTCGTCCTGAGGAGCCCTGAGGTGGGCAGCAGGGGCCAGGGGAAGTTTTCA 206

Qy        824 GGCCTTCATCAAAGAGAACAACATCCTCAGCTCCGCACCCCTCATCCTGTATCAGCACTT 883
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 GGCCTTCATCAAAGAGAACAACATCCTCAGCTCCGCACCCCTCATCCTGTATCAGCACTT 146

Qy        884 ACC-GGTGTGTGACTGCCCTTGTCAGCTAGCATACGGTGGGCCCACCTGGCCCACTGGCT 942
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 ACCNGGTGTGTGACTGCCCTTGTCAGCTAGCATACGGTGGGCCCACCTGGCCCACTGGCT 86

Qy        943 GTTTATGCCACTGATTTATGATAGGGAATATTATCTTTGAACCCAATGAAGTGTTTTCTC 1002
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 GTTTATGCCACTGATTTATGATAGGGAATATTATCTTTGAACCCAATGAAGTGTTTTCTC 26

Qy       1003 CCCCATCACAAAAAAAAAAA 1022
              ||||||||||||||||||||
Db         25 CCCCATCACAAAAAAAAAAA 6


RESULT 9
CD723979
LOCUS       CD723979                611 bp    mRNA    linear   EST 26-JUN-2003
DEFINITION  oj28g08.y1 Human lacrimal gland, unamplified: oj Homo sapiens cDNA
            clone oj28g08 5', mRNA sequence.
ACCESSION   CD723979
VERSION     CD723979.1  GI:32274833
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 611)
  AUTHORS   Dickinson,D., Laurie,G. and Wistow,G.
  TITLE     Expressed sequence tag analysis of human lacrimal gland
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Wistow G
            Section on Molecular Structure and Function
            National Eye Institute
            6/331, NIH, Bethesda, MD 20892-2740, USA
            Tel: 301 402 3452
            Fax: 301 496 0078
            Email: graeme@helix.nih.gov
            Plate: 28  row: g  column: 08
            Seq primer: M13RP1 reverse primer (ABI).
FEATURES              Location/Qualifiers
     source           1. .611
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="oj28g08"
                      /tissue_type="lacrimal gland"
                      /dev_stage="Adult"
                      /lab_host="EMDH10B"
                      /clone_lib="Human lacrimal gland, unamplified: oj"
                      /note="Organ: Eye; Vector: pCMVSport6; RNA was extracted
                      from 2 human lacrimal glands. A directionally cloned cDNA
                      library in the pCMVSPORT6 vector(Life Technologies) was
                      constructed at Bioserve Biotechnology (Laurel MD)
                      essentially following the protocols of the SuperScript
                      Plasmid System full details of which are contained in the
                      manufacturer's Instruction manual
                      (http://www.lifetech.com/). First strand synthesis was
                      carried out using a Not I primer-adapter
                      [5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCC(T)15-3']. EST analysis
                      was performed on the unamplified library at the NIH
                      Intramural Sequencing Center (NISC)."
ORIGIN

  Query Match             21.9%;  Score 604.2;  DB 6;  Length 611;
  Best Local Similarity   99.5%;  Pred. No. 1.1e-147;
  Matches  606;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;
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Qy        167 GCACTGGGCGATGTCCCCAGAGCAGGGCAAGGTCTCTAGAGCGGGTCTCCCACATGACTG 226
              ||||||||||| | ||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCACTGGGCGAGGCCCCCAGAGCAGGGCAAGGTCTCTAGAGCGGGTCTCCCACATGACTG 61

Qy        227 GCTTCACACAGGCACTTCCGCTCGGGTTGCATGCTCTGTGTCATCTTACCGGTCCAGGGT 286
              ||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db         62 GCTTCACACAGGCACTTCCGCTTGGGTTGCATGCTCTGTGTCATCTTACCGGTCCAGGGT 121

Qy        287 TGCAGGTAGGAAATGTTTGTACCCTCTTCTGATTGCCACCTCCTTCCCATCGCCCCTTAG 346
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 TGCAGGTAGGAAATGTTTGTACCCTCTTCTGATTGCCACCTCCTTCCCATCGCCCCTTAG 181

Qy        347 GGACAGGGCTTGAGGGCCAGTGAGGCGCTGGTCAGGCACCCCAGGCCTCCTTGGGACCTG 406
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GGACAGGGCTTGAGGGCCAGTGAGGCGCTGGTCAGGCACCCCAGGCCTCCTTGGGACCTG 241

Qy        407 CCCAGGGGCACCCTGAGAGCTCCTGAAACCCCCACTTAGCTTCCAGACCTTTCTGCAAAA 466
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 CCCAGGGGCACCCTGAGAGCTCCTGAAACCCCCACTTAGCTTCCAGACCTTTCTGCAAAA 301

Qy        467 GCTCCTCCTGGCTTTCCTCCCTCCCCCAATCTATGGGTCACAGCTAACAGATCTGAGGGC 526
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GCTCCTCCTGGCTTTCCTCCCTCCCCCAATCTATGGGTCACAGCTAACAGATCTGAGGGC 361

Qy        527 AACTGCTGTGCTAGTGGCCAGGGCTGCACCTGCCATCCCCGGCTCTGCCACTTTAGGGCC 586
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 AACTGCTGTGCTAGTGGCCAGGGCTGCACCTGCCATCCCCGGCTCTGCCACTTTAGGGCC 421

Qy        587 TTCTAGAGGCAGTGTCCTTAGGAAGTAGCTCTGAGGCATGGGTTTTCTGCTCCTGTGCAG 646
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 TTCTAGAGGCAGTGTCCTTAGGAAGTAGCTCTGAGGCATGGGTTTTCTGCTCCTGTGCAG 481

Qy        647 GGCAGCTGATGGGATAAGGTGGGGAAGGACGGTCAGTGCTTGGGCCCCAGCTGGCCAGCC 706
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        482 GGCAGCTGATGGGATAAGGTGGGGAAGGACGGTCAGTGCTTGGGCCCCAGCTGGCCAGCC 541

Qy        707 TGGCGATGGGGAAACCAAACCATGTCCCCCAGCGAAGGGCCAGAGTGGGAACCTGTCCTC 766
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        542 TGGCGATGGGGAAACCAAACCATGTCCCCCAGCGAAGGGCCAGAGTGGGAACCTGTCCTC 601

Qy        767 ATGCCCTTC 775
              |||||||||
Db        602 ATGCCCTTC 610


RESULT 10
AI928242/c
LOCUS       AI928242                577 bp    mRNA    linear   EST 08-MAR-2000
DEFINITION  wo95h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463121 3',
            mRNA sequence.
ACCESSION   AI928242
VERSION     AI928242.1  GI:5664206
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 577)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 721   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 453.
FEATURES             Location/Qualifiers
     source          1. .577
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:2463121"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Kid11"
                     /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
                     a modified polylinker; Site_1: Not I; Site_2: Eco RI;
                     Plasmid DNA from the normalized library NCI_CGAP_Kid3 was
                     prepared, and ss circles were made in vitro. Following HAP
                     purification, this DNA was used as tracer in a subtractive
                     hybridization reaction. The driver was PCR-amplified cDNAs
                     from a pool of 5,000 clones made from the same library
                     (cloneIDs 1322376-1323911, 1456007-1456775, and
                     1500552-1502855). Subtraction by Bento Soares and M.
                     Fatima Bonaldo.  "
ORIGIN

  Query Match           20.5%;  Score 563.4;  DB 1;  Length 577;
  Best Local Similarity   99.7%;  Pred. No. 6.5e-137;
  Matches  575;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy       2150 GGTCCCACAGCTACTGATGGCCCGAGCCAGGTTGAGCTTCCTGGTGTCCAGTCCGGATCC 2209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        577 GGTCCCACAGCTACTGATGGCCCGAGCCAGGTTGAGCTTCCTGGTGTCCAGTCCGGATCC 518

Qy       2210 CACTTGCAGATCTCATGCTCTCAGATAGGTGGGACAAGTTCTTTTGTCACAGTGCTGGCT 2269
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        517 CACTTGCAGATCTCATGCTCTCAGATAGGTGGGACAAGTTCTTTTGTCACAGTGCTGGCT 458

Qy       2270 CTGTCCTGAGGCCTCATTGCTGGCTGGGTGTGCTCTGCTGGGAAAAGCTTTGCGGGGCTT 2329
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        457 CTGTCCTGAGGCCTCATTGCTGGCTGGGTGTGCTCTGCTGGGAAAAGCTTTGCGGGGCTT 398

Qy       2330 GCTTGGTTAACCACAGAAGAGAAGGGGACTGTTTGGGGTGCCTCTCTGCAGCCTCCCCGT 2389
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        397 GCTTGGTTAACCACAGAAGAGAAGGGGACTGTTTGGGGTACCTCTCTGCAGCCTCCCCGT 338

Qy       2390 GCTGGGTGGAAGCACGGTTACTGTGTTCTCTAATGTTCATGTATTTAAAATGATTTCTTT 2449
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        337 GCTGGGTGGAAGCACGGTTACTGTGTTCTCTAATGTTCATGTATTTAAAATGATTTCTTT 278

Qy       2450 CTAAAGATGTAACCTCCACACCTTTCTCCAGATTGGGTGACTCTTTTCTAAA-GGTGGTG 2508
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        277 CTAAAGATGTAACCTCCACACCTTTCTCCAGATTGGGTGACTCTTTTCTAAAGGGTGGTG 218

Qy       2509 GGAGTATCTGTCGGGGTGGTGTGGCCCTTGGATGGGTCAGGTGGGTGTGAGAGGTCCTGG 2568
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        217 GGAGTATCTGTCGGGGTGGTGTGGCCCTTGGATGGGTCAGGTGGGTGTGAGAGGTCCTGG 158

Qy       2569 GGAGGTGGGCGTTGAGCTCAAAGTTGTCCTACTGCCATGTTTTTGTACCTGAAATAAAGC 2628
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        157 GGAGGTGGGCGTTGAGCTCAAAGTTGTCCTACTGCCATGTTTTTGTACCTGAAATAAAGC 98

Qy       2629 ATATTTTGCACTTGTTACTGTACCATAGTGCGGACGAGAAGTCTGTATGTGGGATCTGTG 2688
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         97 ATATTTTGCACTTGTTACTGTACCATAGTGCGGACGAGAAGTCTGTATGTGGGATCTGTG 38

Qy       2689 CTTGGGTTAGAATGCAAATAAAACTCACATTTGTAAG 2725
              |||||||||||||||||||||||||||||||||||||
Db         37 CTTGGGTTAGAATGCAAATAAAACTCACATTTGTAAG 1


RESULT 11
BM019092
LOCUS       BM019092                768 bp    mRNA    linear   EST 30-OCT-2001
DEFINITION  603647129F1 NIH_MGC_98 Homo sapiens cDNA clone IMAGE:5428711 5',
            mRNA sequence.
ACCESSION   BM019092
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VERSION     BM019092.1  GI:16533446
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 768)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1896  row: j  column: 08
            High quality sequence stop: 578.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5428711"
                     /tissue_type="astrocytoma grade IV, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_98"
                     /note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Library constructed  by Ling Hong
                     in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             20.4%;  Score 562.8;  DB 4;  Length 768;
  Best Local Similarity   94.8%;  Pred. No. 1e-136;
  Matches  626;  Conservative    0;  Mismatches   27;  Indels    7;  Gaps    4;

Qy       1174 ACCGTCTAGCCCGTTACAGAAAAAGTCTGCTGACTACTGAGCCAGACCTCCATTACCTCC 1233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 ACCGTCTAGCCCGTTACAGAAAAAGTCTGCTGACTACTGAGCCAGACCTCCATTACCTCC 61

Qy       1234 ATCCCTGTTGGATTATTTAAAGAAAGCCTCAGACAGTAAGGGCTTTTTAAAAGAATAAA 1293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 ATCCCTGTTGGATTATTTAAAGAAAGCCTCAGACAGTAAGGGCTTTTTAAAAGAATAAA 121

Qy       1294 ATGACTTGGTTTGCGCTTGGAAGCAGGGGAAGCATTCAGATGAGCGGTTTCTGCATTAAC 1353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 ATGACTTGGTTTGCGCTTGGAAGCAGGGGAAGCATTCAGATGAGCGGTTTCTGCATTAAC 181

Qy       1354 CCTGCCTATCACGCATCTCGTGTCCTGTGTGGCTGGCGAGCCCCCCTTGGAAGGTTCTGG 1413
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CCTGCCTATCACGCATCTCGTGTCCTGTGTGGCTGGCGAGCCCCCCTTGGAAGGTTCTGG 241

Qy       1414 TGCTTCAGCTGGCTCCTGCAGAGTCCACCCCGCCTCGTGGTGGGAATGCAGAGCCCTTTG 1473
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 TGCTTCAGCTGGCTCCTGCAGAGTCCACCCCGCCTCGTGGTGGGAATGCAGAGCCCTTTG 301

Qy       1474 CTTTCCTTCTTGCCGCCTGCTTCCTGTTCCTGGGGACCCGCTGGGCCTTTGGTCTGCATC 1533
              ||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db        302 CTTTCCTTCTTGCCAGCTGCTTCCTGTTCCTGGGGACCCGCTGGGCCTTTGGTCTGCATC 361

Qy       1534 CCCTGGCCAGGTCCCTCAGGG-TTGATGCGTGGAGAA-GGACTTTGAGCAGTGGTGGGCA 1591
              ||||||||||||||||||||| ||||||||||||||| ||||||||||||||||||||||
Db        362 CCCTGGCCAGGTCCCTCAGGGATTGATGCGTGGAGAACGGACTTTGAGCAGTGGTGGGCA 421

Qy       1592 GCAGTGGCCTCCTGGCCAGCTCACACTCTTGTCCTGGGAGGGGCAGCCTGATCTCACCTC 1651
              ||||||||||||||||||| ||| ||||| |||||||||||||||||||||||||| |||
Db        422 GCAGTGGCCTCCTGGCCAGATCAAACTCTAGTCCTGGGAGGGGCAGCCTGATCTCAACTC 481

Qy       1652 CACCTAGTACCTTGGGGACTGAGGACCTTTTGGCTTCTCTGGAGCCTGCAAGCCTCTTCC 1711
              || ||||||||||||||||||||||||||| ||||||||||||||||||||| |||||||
Db        482 CAACTAGTACCTTGGGGACTGAGGACCTTTAGGCTTCTCTGGAGCCTGCAAGACTCTTCC 541

Qy       1712 CATGTGTCCAGCTGCTCTTCCTGCTACAAAGGGGACTGCTCAC-AGTGGCCTCAGCTTGG 1770
              |||||||||||||||||||||||||||||||||||||| |||| ||||| |||||||||
Db        542 CATGTGTCCAGCTGCTCTTCCTGCTACAAAGGGGACTGATCACAAGTGGACTCAGCTTGA 601

Qy       1771 TGGTTTTGAGGGGCCGCC----CCCCGGCCCTCCATAAGGGTATCCTGGGCCTGAGAATT 1826
                |       | |  |||    | |||| ||||||||||||||||||||||||||||| |
Db        602 AAGGAAAAGAGAGGAGCCGACACACCGGACCTCCATAAGGGTATCCTGGGCCTGAGAACT 661


RESULT 12
BU678926
LOCUS       BU678926                 577 bp    mRNA    linear   EST 07-OCT-2002
DEFINITION  UI-CF-DU1-abc-n-17-0-UI.s1 UI-CF-DU1 Homo sapiens cDNA clone
            UI-CF-DU1-abc-n-17-0-UI 3', mRNA sequence.
ACCESSION   BU678926
VERSION     BU678926.1  GI:23526358
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 577)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
   PUBMED   8889548
COMMENT     Contact: McCray, PB
            McCray Lab
            University of Iowa
            2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
            Tel: 319 356 4866
            Fax: 319 356 7171
            Email: paul-mccray@uiowa.edu
            Tissue Procurement: Dr. M. J. Welsh, University of Iowa
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com) or from Open Biosystems
            (www.openbiosystems.com).
             The following repetitive elements were found in this cDNA
            sequence: 188-250, >MER58B#DNA/MER1_type (matched compliment)
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1..577
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-CF-DU1-abc-n-17-0-UI"
                     /tissue_type="Primary Lung Epithelial Cells"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                     /clone_lib="UI-CF-DU1"
                     /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     UI-CF-DU1 is a normalized cDNA library containing the
                     following tissue(s): Primary Lung Epithelial Cells The
                     library was constructed according to Bonaldo, Lennon and
                     Soares, Genome Research, 6:791-806, 1996. First strand
                     cDNA synthesis was primed with an oligo-dT primer
                     containing a Not I site.  Double stranded cDNA was ligated
                     to an EcoR I adaptor, digested with Not I, and cloned
                     directionally into pT7T3-Pac vector. The oligonucleotide
```

used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCTGTAGGC.
TAG_TISSUE=Lung Epithelial Cells Tissue nos 359-368
TAG_LIB=UI-CF-DU1
TAG_SEQ=GGCTGTAGGC"

ORIGIN

Query Match 20.3%; Score 560.2; DB 5; Length 577;
Best Local Similarity 99.5%; Pred. No. 4.6e-136;
Matches 562; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy        971 TATTATCTTTGAACCCAATGAAGTGTTTTCTCCCCCATCACAAAAAAAAAAAATTCTTATT 1030
              |||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db          9 TTTTATCTTTGAACCCAATGACATGTTTTCTCCCCCATCACAAAAAAAAAAAATTCTTATT 68

Qy       1031 TTTAGTAGACATGTATTTACCAAAAATATGTACTCAATTATTGTATTTTGGATTTTATCA 1090
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 TTTAGTAGACATGTATTTACCAAAAATATGTACTCAATTATTGTATTTTGGATTTTATCA 128

Qy       1091 ATTTAAAAATTGTGGAAATTTGTTTGCTCTTACGCCAACATAATATTGATTTTGCCTCTT 1150
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 ATTTAAAAATTGTGGAAATTTGTTTGCTCTTACGCCAACATAATATTGATTTTGCCTCTT 188

Qy       1151 GGCTCTGAAAGCCCAAAATATTTACCGTCTAGCCCGTTACAGAAAAAGTCTGCTGACTAC 1210
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 GGCTCTGAAAGCCCAAAATATTTACCGTCTAGCCCGTTACAGAAAAAGTCTGCTGACTAC 248

Qy       1211 TGAGCCAGACCTCCATTACCTCCATCCCTGTTGGATTATTTAAAGAAAGCCTCAGACAGT 1270
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 TGAGCCAGACCTCCATTACCTCCATCCCTGTTGGATTATTTAAAGAAAGCCTCAGACAGT 308

Qy       1271 AAGGGCTTTTTTAAAAGAATAAAATGACTTGGTTTGCGCTTGGAAGCAGGGGAAGCATTC 1330
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Db        309 AAGGGCTTTTTTAAAAGAATAAAATGACTTGGTTTGCGCTTGGAAGCAGGGGAAGCATTC 368

Qy       1331 AGATGAGCGGTTTCTGCATTAACCCTGCCTATCACGCATCTCGTGTCCTGTGTGGCTGGC 1390
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 AGATGAGCGGTTTCTGCATTAACCCTGCCTATCACGCATCTCGTGTCCTGTGTGGCTGGC 428

Qy       1391 GAGCCCCCCTTGGAAGGTTCTGGTGCTTCAGCTGGCTCCTGCAGAGTCCACCCCGCCTCG 1450
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Db        429 GAGCCCCCCTTGGAAGGTTCTGGTGCTTCAGCTGGCTCCTGCAGAGTCCACCCCGCCTCG 488

Qy       1451 TGGTGGGAATGCAGAGCCCTTTGCTTTCCTTCTTGCCGCCTGCTTCCTGTTCCTGGGGAC 1510
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Db        489 TGGTGGGAATGCAGAGCCCTTTGCTTTCCTTCTTGCCGCCTGCTTCCTGTTCCTGGGGAC 548

Qy       1511 CCGCTGGGCCTTTGGTCTGCATCCC 1535
              |||||||||||||||||||||||||
Db        549 CCGCTGGGCCTTTGGTCTGCATCCC 573
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RESULT 13
AW271767/c
LOCUS AW271767 547 bp mRNA linear EST 03-JAN-2000
DEFINITION xs18a11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2769980 3', mRNA sequence.
ACCESSION AW271767
VERSION AW271767.1 GI:6658797
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 547)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 443.
FEATURES Location/Qualifiers
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/mol_type="mRNA"
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/clone="IMAGE:2769980"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Kid11"
/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo. "
ORIGIN

Query Match 19.8%; Score 546; DB 2; Length 547;
Best Local Similarity 99.8%; Pred. No. 2.5e-132;
Matches 546; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       2179 GGTTGAGCTTCCTGGTGTCCAGTCCGGATCCCACTTGCAGATCTCATGCTCTCAGATAGG 2238
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Db        547 GGTTGAGCTTCNTGGTGTCCAGTCCGGATCCCACTTGCAGATCTCATGCTCTCAGATAGG 488

Qy       2239 TGGGACAAGTTCTTTTGTCACAGTGCTGGCTCTGTCCTGAGGCCTCATTGCTGGCTGGGT 2298
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Db        487 TGGGACAAGTTCTTTTGTCACAGTGCTGGCTCTGTCCTGAGGCCTCATTGCTGGCTGGGT 428

Qy       2299 GTGCTCTGCTGGGAAAAGCTTTGCGGGGCTTGCTTGGTTAACCACAGAAGAGAAGGGGAC 2358
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Db        427 GTGCTCTGCTGGGAAAAGCTTTGCGGGGCTTGCTTGGTTAACCACAGAAGAGAAGGGGAC 368

Qy       2359 TGTTTGGGGTGCCTCTCTGCAGCCTCCCCGTGCTGGGTGGAAGCACGGTTACTGTGTTCT 2418
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Db        367 TGTTTGGGGTGCCTCTCTGCAGCCTCCCCGTGCTGGGTGGAAGCACGGTTACTGTGTTCT 308

Qy       2419 CTAATGTTCATGTATTTAAAATGATTTCTTTCTAAAGATGTAACCTCCACACCTTTCTCC 2478
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Db        307 CTAATGTTCATGTATTTAAAATGATTTCTTTCTAAAGATGTAACCTCCACACCTTTCTCC 248

Qy       2479 AGATTGGGTGACTCTTTTCTAAAGGTGGTGGGAGTATCTGTCGGGGTGGTGTGGCCCTTG 2538
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Db        247 AGATTGGGTGACTCTTTTCTAAAGGTGGTGGGAGTATCTGTCGGGGTGGTGTGGCCCTTG 188

Qy       2539 GATGGGTCAGGTGGGTGTGAGAGGTCCTGGGGAGGTGGGCGTTGAGCTCAAAGTTGTCCT 2598
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Db        187 GATGGGTCAGGTGGGTGTGAGAGGTCCTGGGGAGGTGGGCGTTGAGCTCAAAGTTGTCCT 128

Qy       2599 ACTGCCATGTTTTTGTACCTGAAATAAAGCATATTTTGCACTTGTTACTGTACCATAGTG 2658
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Db        127 ACTGCCATGTTTTTGTACCTGAAATAAAGCATATTTTGCACTTGTTACTGTACCATAGTG 68

Qy       2659 CGGACGAGAAGTCTGTATGTGGGATCTGTGCTTGGGTTAGAATGCAAATAAAACTCACAT 2718
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 CGGACGAGAAGTCTGTATGTGGGATCTGTGCTTGGGTTAGAATGCAAATAAAACTCACAT 8

Qy       2719 TTGTAAG 2725
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Db           7 TTGTAAG 1
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RESULT 14
AW173671/c
LOCUS       AW173671                 535 bp    mRNA    linear   EST 16-NOV-1999
DEFINITION  xj10g08.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2656862 3',
            mRNA sequence.
ACCESSION   AW173671
VERSION     AW173671.1  GI:6439619
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 535)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: -40UP from Gibco
            High quality sequence stop: 420.
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                     adenocarcinoma, 3 pooled tumors"
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                     /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;
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                     Average insert size 1.85 kb. Life Technologies catalog #:
                     11539-012"
ORIGIN

  Query Match             19.3%;  Score 532.4;  DB 2;  Length 535;
  Best Local Similarity   99.6%;  Pred. No. 9.6e-129;
  Matches  533;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2191 TGGTGTCCAGTCCGGATCCCACTTGCAGATCTCATGCTCTCAGATAGGTGGGACAAGTTC 2250
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Qy       2251 TTTTGTCACAGTGCTGGCTCTGTCCTGAGGCCTCATTGCTGGCTGGGTGTGCTCTGCTGG 2310
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        475 TTTTGTCACAGTGCTGGCTCTGTCCTGAGGCCTCATTGCTGGCTGGGTGTGCTCTGCTGG 416

Qy       2311 GAAAAGCTTTGCGGGGCTTGCTTGGTTAACCACAGAAGAGAAGGGGACTGTTTGGGGTGC 2370
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Qy       2371 CTCTCTGCAGCCTCCCCGTGCTGGGTGGAAGCACGGTTACTGTGTTCTCTAATGTTCATG 2430
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Db        355 CTCTCTGCAGCCTCCCCGTGCTGGGTGGAAGCACGGTTACTGTGTTCTCTAATGTTCATG 296

Qy       2431 TATTTAAAATGATTTCTTTCTAAAGATGTAACCTCCACACCTTTCTCCAGATTGGGTGAC 2490
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Qy       2551 GGGTGTGAGAGGTCCTGGGGAGGTGGGCGTTGAGCTCAAAGTTGTCCTACTGCCATGTTT 2610
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Db          55 CTGTATGTGGGATCTGTGCTTGGGTTAGAATGCAAATAAAACTCACATTTGTAAG 1


RESULT 15
AW195353/c
LOCUS       AW195353                 538 bp    mRNA    linear   EST 29-NOV-1999
DEFINITION  xn37d01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2695873 3',
            mRNA sequence.
ACCESSION   AW195353
VERSION     AW195353.1  GI:6474429
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 538)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: -40UP from Gibco
            High quality sequence stop: 464.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:2695873"
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                     /clone_lib="NCI_CGAP_Kid11"
                     /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
                     a modified polylinker; Site_1: Not I; Site_2: Eco RI;
                     Plasmid DNA from the normalized library NCI_CGAP_Kid3 was
                     prepared, and ss circles were made in vitro. Following HAP
                     purification, this DNA was used as tracer in a subtractive
                     hybridization reaction. The driver was PCR-amplified cDNAs
                     from a pool of 5,000 clones made from the same library
                     (cloneIDs 1322376-1323911, 1456007-1456775, and
                     1500552-1502855). Subtraction by Bento Soares and M.
                     Fatima Bonaldo.  "
ORIGIN

  Query Match             19.1%;  Score 526;  DB 2;  Length 538;
  Best Local Similarity   99.8%;  Pred. No. 4.7e-127;
  Matches  537;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

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Db        538 TGGCTTTCCTCCCTCCCCCAATCTATGGGTCACAGCTAACAGATCTGAGGGCAACTGCTG 479

Qy        535 TGCTAGTGGCCAGGGCTGCACCTGCCATCCCCGGCTCTGCCACTTTAGGGCCTTCTAGAG 594
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Db           478 TGCTAGTGGCCAGGGCTGCACCTGCCATCCCCGGCTCTGCCACTTTAGGGCCTTCTAGAG 419

Qy           595 GCAGTGTCCTTAGGAAGTAGCTCTGAGGCATGGGTTTTCTGCTCCTGTGCAGGGCAGCTG 654
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           418 GCAGTGTCCTTAGGAAGTAGCTCTGAGGCATGGGTTTTCTGCTCCTGTGCAGGGCAGCTG 359

Qy           655 ATGGGATAAGGTGGGGAAGGACGGTCAGTGCTTGGGCCCCAGCTGGCCAGCCTGGCGATG 714
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Db           358 ATGGGATAAGGTGGGGAAGGACGGTCAGTGCTTGGGCCCCAGCTGGCCAGCCTGGCGATG 299

Qy           715 GGGAAACCAAACCATGTCCCCCAGCGAAGGGCCAGAGTGGGAACCTGTCCTCATGCCCTT 774
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Db           298 GGGAAACCAAACCATGTCCCCCAGCGAAGGGCCAGAGTGGGAACCTGTCCTCATGCCCTT 239

Qy           775 CGTCCTGAGGAGCCCTGAGGTGGGCAGCAGGGGCCAGGGGAAGTTTTCAGGCCTTCATCA 834
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Db           178 AAGAGAACAACATCCTCAGCTCCGCACCCCTCATCCTGTATCAGCACTTACCGGTGTGTG 119

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Search completed: November 29, 2004, 14:15:24
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: November 29, 2004, 08:42:07 ; Search time 2334 Seconds
(without alignments)
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Perfect score: 2754
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3640242 seqs, 2709731945 residues

Total number of hits satisfying chosen parameters: 7280484

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	2754	100.0	2754	9	US-09-989-920-100	Sequence 100, App
	2	2754	100.0	2754	14	US-10-074-475-2	Sequence 2, Appli
c	3	2397.4	87.1	2399	9	US-09-989-920-91	Sequence 91, Appl
	4	612.4	22.2	960	9	US-09-989-920-99	Sequence 99, Appl
c	5	524	19.0	524	15	US-10-172-118-2364	Sequence 2364, Ap
c	6	524	19.0	524	16	US-10-342-887-2364	Sequence 2364, Ap
	7	483.8	17.6	591	14	US-10-074-475-1	Sequence 1, Appli
	8	357.4	13.0	395	16	US-10-609-021-176	Sequence 176, App
	9	295	10.7	295	15	US-10-116-712-429	Sequence 429, App
c	10	224.4	8.1	251	9	US-09-989-920-90	Sequence 90, Appl
c	11	161	5.8	161	15	US-10-102-524-1276	Sequence 1276, Ap
	12	93.6	3.4	2285	10	US-09-854-867-10	Sequence 10, Appl
c	13	75	2.7	32038	9	US-09-764-878-292	Sequence 292, App
c	14	75	2.7	32038	14	US-10-079-854-292	Sequence 292, App
	15	75	2.7	32844	11	US-09-984-429-498	Sequence 498, App
c	16	75	2.7	72678	17	US-10-322-281-214	Sequence 214, App
	17	70.8	2.6	10410	17	US-10-302-027-4	Sequence 4, Appli
c	18	66	2.4	215221	13	US-10-087-192-1360	Sequence 1360, Ap
c	19	65.2	2.4	248436	13	US-10-087-192-2014	Sequence 2014, Ap
	20	62.8	2.3	494	13	US-10-027-632-320960	Sequence 320960,
	21	62.8	2.3	494	15	US-10-027-632-320960	Sequence 320960,
	22	62.8	2.3	498	13	US-10-027-632-96975	Sequence 96975, A
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ALIGNMENTS

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; Sequence 100, Application US/09989920
; Patent No. US20020172957A1
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herve
; APPLICANT: Chen, Sei-Yu
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prote
; FILE REFERENCE: DEX-0291
; CURRENT APPLICATION NUMBER: US/09/989,920
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/252,500
; PRIOR FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 284
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 100
; LENGTH: 2754
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-989-920-100

Query Match 100.0%; Score 2754; DB 9; Length 2754;
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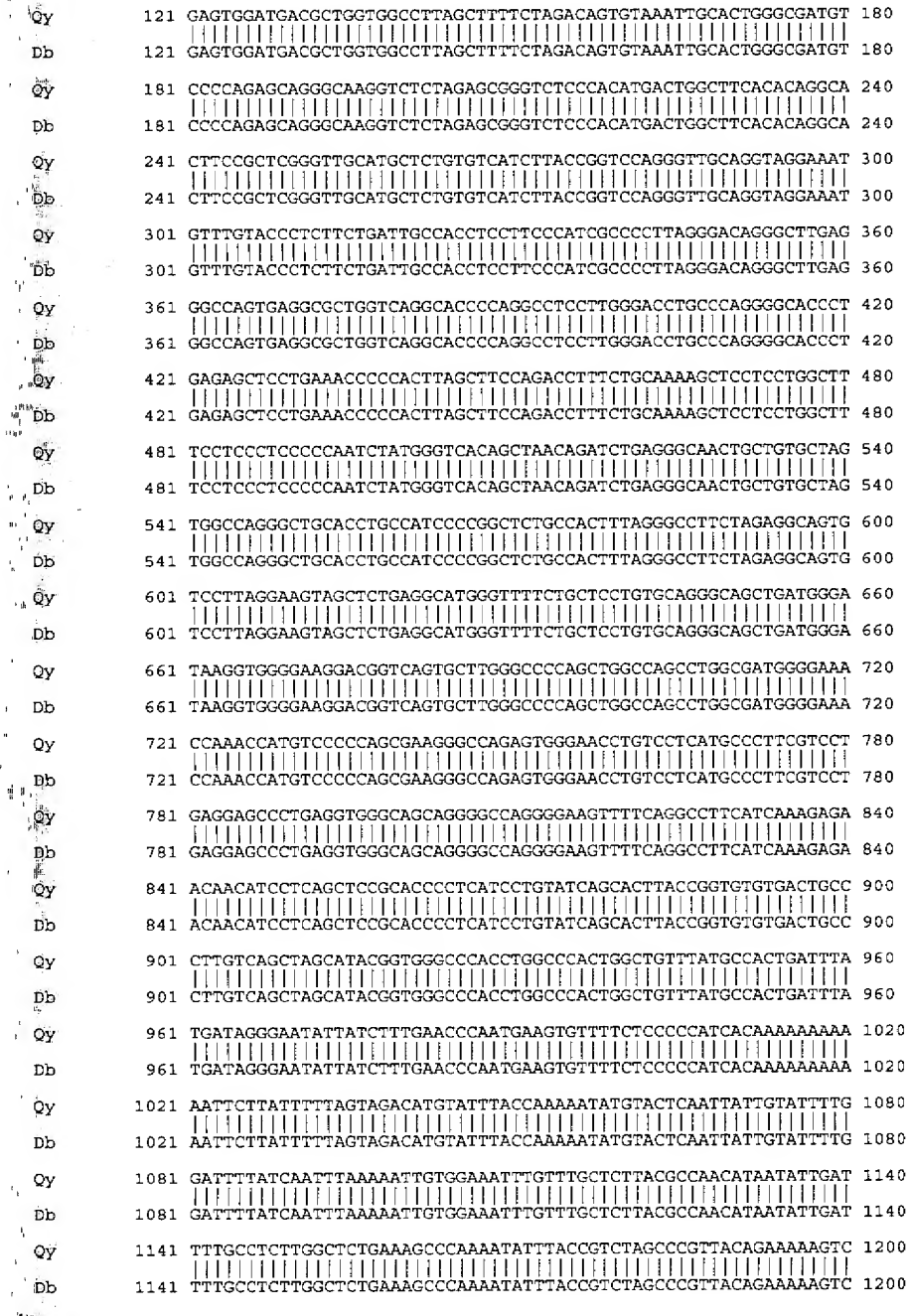
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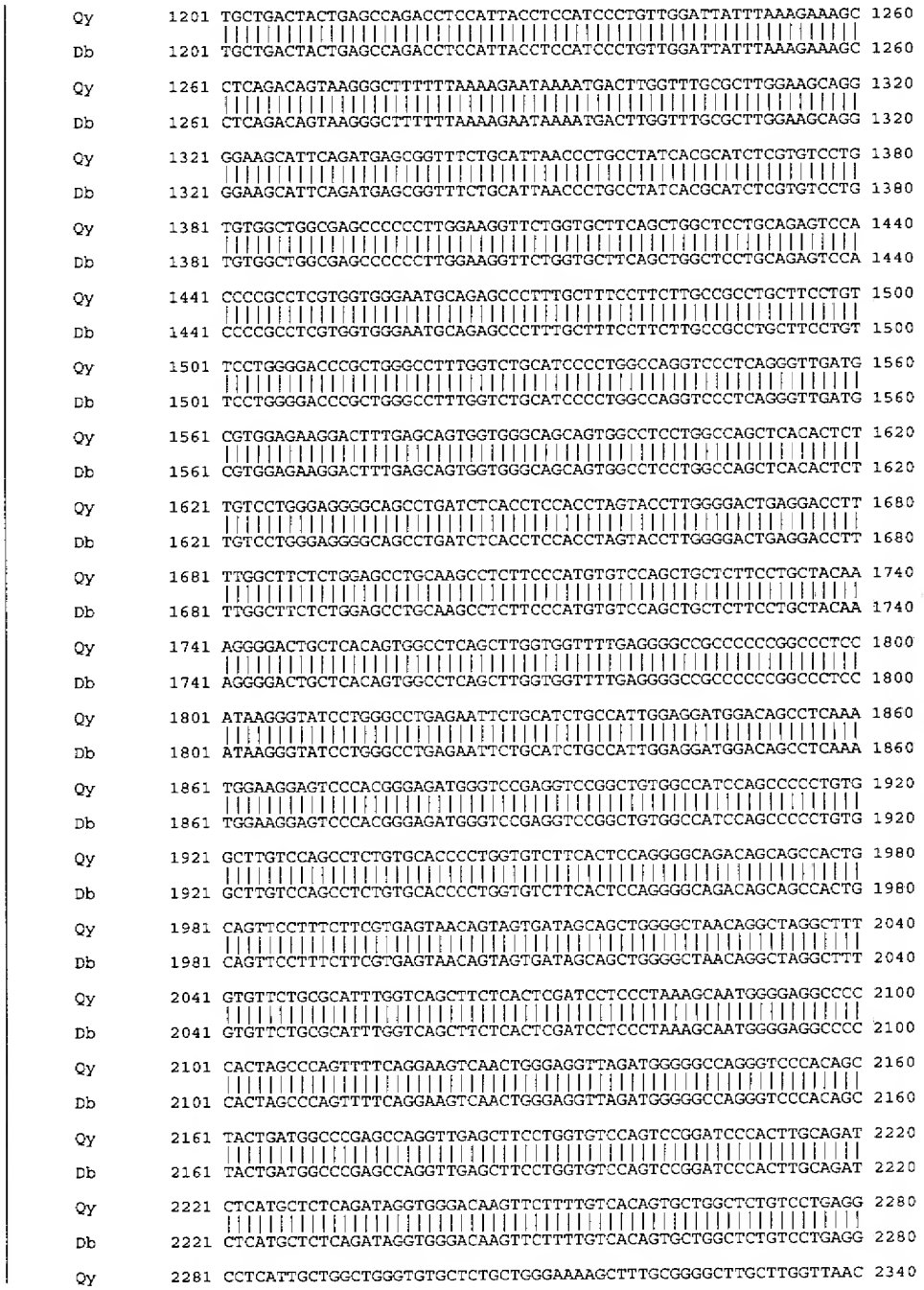
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; Publication No. US20030092898A1
; GENERAL INFORMATION:
;  APPLICANT: Salceda, Susana
;  APPLICANT:  Macina, Roberto
;  APPLICANT:  Hu, Ping
;  APPLICANT:  Recipon, Herve
;  APPLICANT:  Karra, Kalpana
;  APPLICANT:  Cafferkey, Robert
;  APPLICANT:  Sun, Yongming
;  APPLICANT:  Liu, Chenghua
;  TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific
;  TITLE OF INVENTION:  Genes and Proteins
;  FILE REFERENCE: DEX-0313
;  CURRENT APPLICATION NUMBER: US/10/074,475
;  CURRENT FILING DATE:  2002-02-13
;  PRIOR APPLICATION NUMBER: 60/268,292
;  PRIOR FILING DATE: 2001-02-13
;  NUMBER OF SEQ ID NOS: 295
;  SOFTWARE: PatentIn version 3.1
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US-10-074-475-2

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Qy       1681 TTGGCTTCTCTGGAGCCTGCAAGCCTCTTCCCATGTGTCCAGCTGCTCTTCCTGCTACAA 1740
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Db       1681 TTGGCTTCTCTGGAGCCTGCAAGCCTCTTCCCATGTGTCCAGCTGCTCTTCCTGCTACAA 1740

Qy       1741 AGGGGACTGCTCACAGTGGCCTCAGCTTGGTGGTTTTGAGGGGCCGCCCCCCGGCCCTCC 1800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 AGGGGACTGCTCACAGTGGCCTCAGCTTGGTGGTTTTGAGGGGCCGCCCCCCGGCCCTCC 1800

Qy       1801 ATAAGGGTATCCTGGGCCTGAGAATTCTGCATCTGCCATTGGAGGATGGACAGCCTCAAA 1860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 ATAAGGGTATCCTGGGCCTGAGAATTCTGCATCTGCCATTGGAGGATGGACAGCCTCAAA 1860

Qy       1861 TGGAAGGAGTCCCACGGGAGATGGGTCCGAGGTCCGGCTGTGGCCATCCAGCCCCCTGTG 1920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 TGGAAGGAGTCCCACGGGAGATGGGTCCGAGGTCCGGCTGTGGCCATCCAGCCCCCTGTG 1920

Qy       1921 GCTTGTCCAGCCTCTGTGCACCCCTGGTGTCTTCACTCCAGGGGCAGACAGCAGCCACTG 1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 GCTTGTCCAGCCTCTGTGCACCCCTGGTGTCTTCACTCCAGGGGCAGACAGCAGCCACTG 1980

Qy       1981 CAGTTCCTTTCTTCGTGAGTAACAGTAGTGATAGCAGCTGGGGCTAACAGGCTAGGCTTT 2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 CAGTTCCTTTCTTCGTGAGTAACAGTAGTGATAGCAGCTGGGGCTAACAGGCTAGGCTTT 2040

Qy       2041 GTGTTCTGCGCATTTGGTCAGCTTCTCACTCGATCCTCCCTAAAGCAATGGGGAGGCCCC 2100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 GTGTTCTGCGCATTTGGTCAGCTTCTCACTCGATCCTCCCTAAAGCAATGGGGAGGCCCC 2100

Qy       2101 CACTAGCCCAGTTTTCAGGAAGTCAACTGGGAGGTTAGATGGGGGCCAGGGTCCCACAGC 2160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 CACTAGCCCAGTTTTCAGGAAGTCAACTGGGAGGTTAGATGGGGGCCAGGGTCCCACAGC 2160

Qy       2161 TACTGATGGCCCGAGCCAGGTTGAGCTTCCTGGTGTCCAGTCCGGATCCCACTTGCAGAT 2220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 TACTGATGGCCCGAGCCAGGTTGAGCTTCCTGGTGTCCAGTCCGGATCCCACTTGCAGAT 2220

Qy       2221 CTCATGCTCTCAGATAGGTGGGACAAGTTCTTTTGTCACAGTGCTGGCTCTGTCCTGAGG 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 CTCATGCTCTCAGATAGGTGGGACAAGTTCTTTTGTCACAGTGCTGGCTCTGTCCTGAGG 2280

Qy       2281 CCTCATTGCTGGCTGGGTGTGCTCTGCTGGGAAAAGCTTTGCGGGGCTTGCTTGGTTAAC 2340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 CCTCATTGCTGGCTGGGTGTGCTCTGCTGGGAAAAGCTTTGCGGGGCTTGCTTGGTTAAC 2340
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Qy       2341 CACAGAAGAGAAGGGGACTGTTTGGGGTGCCTCTCTGCAGCCTCCCCGTGCTGGGTGGAA 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 CACAGAAGAGAAGGGGACTGTTTGGGGTGCCTCTCTGCAGCCTCCCCGTGCTGGGTGGAA 2400

Qy       2401 GCACGGTTACTGTGTTCTCTAATGTTCATGTATTTAAAATGATTTCTTTCTAAAGATGTA 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 GCACGGTTACTGTGTTCTCTAATGTTCATGTATTTAAAATGATTTCTTTCTAAAGATGTA 2460

Qy       2461 ACCTCCACACCTTTCTCCAGATTGGGTGACTCTTTTCTAAAGGTGGTGGGAGTATCTGTC 2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 ACCTCCACACCTTTCTCCAGATTGGGTGACTCTTTTCTAAAGGTGGTGGGAGTATCTGTC 2520

Qy       2521 GGGGTGGTGTGGCCCTTGGATGGGTCAGGTGGGTGTGAGAGGTCCTGGGGAGGTGGGCGT 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 GGGGTGGTGTGGCCCTTGGATGGGTCAGGTGGGTGTGAGAGGTCCTGGGGAGGTGGGCGT 2580

Qy       2581 TGAGCTCAAAGTTGTCCTACTGCCATGTTTTTGTACCTGAAATAAAGCATATTTTGCACT 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 TGAGCTCAAAGTTGTCCTACTGCCATGTTTTTGTACCTGAAATAAAGCATATTTTGCACT 2640

Qy       2641 TGTTACTGTACCATAGTGCGGACGAGAAGTCTGTATGTGGGATCTGTGCTTGGGTTAGAA 2700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 TGTTACTGTACCATAGTGCGGACGAGAAGTCTGTATGTGGGATCTGTGCTTGGGTTAGAA 2700

Qy       2701 TGCAAATAAAACTCACATTTGTAAGAAAAAAAAAAAAAAATAAAAAGATGCGGCC 2754
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Db       2701 TGCAAATAAAACTCACATTTGTAAGAAAAAAAAAAAAAATAAAAAGATGCGGCC 2754
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RESULT 3
US-09-989-920-91/c
; Sequence 91, Application US/09989920
; Patent No. US20020172957A1
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herve
; APPLICANT: Chen, Sei-Yu
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prote
; FILE REFERENCE: DEX-0291
; CURRENT APPLICATION NUMBER: US/09/989,920
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/252,500
; PRIOR FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 284
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 91
; LENGTH: 2399
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-989-920-91

Query Match 87.1%; Score 2397.4; DB 9; Length 2399;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2398; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy        356 TTGAGGGCCAGTGAGGCGCTGGTCAGGCACCCCAGGCCTCCTTGGGACCTGCCCAGGGGC 415
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db       2399 TTGAGGGCCAGTGAGGTGCTGGTCAGGCACCCCAGGCCTCCTTGGGACCTGCCCAGGGGC 2340

Qy        416 ACCCTGAGAGCTCCTGAAACCCCCACTTAGCTTCCAGACCTTTCTGCAAAAGCTCCTCCT 475
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2339 ACCCTGAGAGCTCCTGAAACCCCCACTTAGCTTCCAGACCTTTCTGCAAAAGCTCCTCCT 2280

Qy        476 GGCTTTCCTCCCTCCCCCAATCTATGGGTCACAGCTAACAGATCTGAGGGCAACTGCTGT 535
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2279 GGCTTTCCTCCCTCCCCCAATCTATGGGTCACAGCTAACAGATCTGAGGGCAACTGCTGT 2220

Qy        536 GCTAGTGGCCAGGGCTGCACCTGCCATCCCCGGCTCTGCCACTTTAGGGCCTTCTAGAGG 595
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2219 GCTAGTGGCCAGGGCTGCACCTGCCATCCCCGGCTCTGCCACTTTAGGGCCTTCTAGAGG 2160
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Qy       596 CAGTGTCCTTAGGAAGTAGCTCTGAGGCATGGGTTTTCTGCTCCTGTGCAGGGCAGCTGA 655
Db      2159 CAGTGTCCTTAGGAAGTAGCTCTGAGGCATGGGTTTTCTGCTCCTGTGCAGGGCAGCTGA 2100

Qy       656 TGGGATAAGGTGGGGAAGGACGGTCAGTGCTTGGGCCCCAGCTGGCCAGCCTGGCGATGG 715
Db      2099 TGGGATAAGGTGGGGAAGGACGGTCAGTGCTTGGGCCCCAGCTGGCCAGCCTGGCGATGG 2040

Qy       716 GGAAACCAAACCATGTCCCCCAGCGAAGGGCCAGAGTGGGAACCTGTCCTCATGCCCTTC 775
Db      2039 GGAAACCAAACCATGTCCCCCAGCGAAGGGCCAGAGTGGGAACCTGTCCTCATGCCCTTC 1980

Qy       776 GTCCTGAGGAGCCCTGAGGTGGGCAGCAGGGGCCAGGGGAAGTTTTCAGGCCTTCATCAA 835
Db      1979 GTCCTGAGGAGCCCTGAGGTGGGCAGCAGGGGCCAGGGGAAGTTTTCAGGCCTTCATCAA 1920

Qy       836 AGAGAACAACATCCTCAGCTCCGCACCCCTCATCCTGTATCAGCACTTACCGGTGTGTGA 895
Db      1919 AGAGAACAACATCCTCAGCTCCGCACCCCTCATCCTGTATCAGCACTTACCGGTGTGTGA 1860

Qy       896 CTGCCCTTGTCAGCTAGCATACGGTGGGCCCACCTGGCCCACTGGCTGTTTATGCCACTG 955
Db      1859 CTGCCCTTGTCAGCTAGCATACGGTGGGCCCACCTGGCCCACTGGCTGTTTATGCCACTG 1800

Qy       956 ATTTATGATAGGGAATATTATCTTTGAACCCAATGAAGTGTTTTCTCCCCCATCACAAAA 1015
Db      1799 ATTTATGATAGGGAATATTATCTTTGAACCCAATGAAGTGTTTTCTCCCCCATCACAAAA 1740

Qy      1016 AAAAAAATTCTTATTTTTAGTAGACATGTATTTACCAAAAATATGTACTCAATTATTGTA 1075
Db      1739 AAAAAAATTCTTATTTTTAGTAGACATGTATTTACCAAAAATATGTACTCAATTATTGTA 1680

Qy      1076 TTTTGGATTTTATCAATTTAAAAATTGTGGAAATTTGTTTGCTCTTACGCCAACATAATA 1135
Db      1679 TTTTGGATTTTATCAATTTAAAAATTGTGGAAATTTGTTTGCTCTTACGCCAACATAATA 1620

Qy      1136 TTGATTTTGCCTCTTGGCTCTGAAAGCCCAAAATATTTACCGTCTAGCCCGTTACAGAAA 1195
Db      1619 TTGATTTTGCCTCTTGGCTCTGAAAGCCCAAAATATTTACCGTCTAGCCCGTTACAGAAA 1560

Qy      1196 AAGTCTGCTGACTACTGAGCCAGACCTCCATTACCTCCATCCCTGTTGGATTATTTAAAG 1255
Db      1559 AAGTCTGCTGACTACTGAGCCAGACCTCCATTACCTCCATCCCTGTTGGATTATTTAAAG 1500

Qy      1256 AAAGCCTCAGACAGTAAGGGCTTTTTTAAAAGAATAAAATGACTTGGTTTGCGCTTGGAA 1315
Db      1499 AAAGCCTCAGACAGTAAGGGCTTTTTTAAAAGAATAAAATGACTTGGTTTGCGCTTGGAA 1440

Qy      1316 GCAGGGGAAGCATTCAGATGAGCGGTTTCTGCATTAACCCTGCCTATCACGCATCTCGTG 1375
Db      1439 GCAGGGGAAGCATTCAGATGAGCGGTTTCTGCATTAACCCTGCCTATCACGCATCTCGTG 1380

Qy      1376 TCCTGTGTGGCTGGCGAGCCCCCCTTGGAAGGTTCTGGTGCTTCAGCTGGCTCCTGCAGA 1435
Db      1379 TCCTGTGTGGCTGGCGAGCCCCCCTTGGAAGGTTCTGGTGCTTCAGCTGGCTCCTGCAGA 1320

Qy      1436 GTCCACCCCGCCTCGTGGTGGGAATGCAGAGCCCTTTGCTTTCCTTCTTGCCGCCTGCTT 1495
Db      1319 GTCCACCCCGCCTCGTGGTGGGAATGCAGAGCCCTTTGCTTTCCTTCTTGCCGCCTGCTT 1260

Qy      1496 CCTGTTCCTGGGGACCCGCTGGGCCTTTGGTCTGCATCCCCTGGCCAGGTCCCTCAGGGT 1555
Db      1259 CCTGTTCCTGGGGACCCGCTGGGCCTTTGGTCTGCATCCCCTGGCCAGGTCCCTCAGGGT 1200

Qy      1556 TGATGCGTGGAGAAGGACTTTGAGCAGTGGTGGGCAGCAGTGGCCTCCTGGCCAGCTCAC 1615
Db      1199 TGATGCGTGGAGAAGGACTTTGAGCAGTGGTGGGCAGCAGTGGCCTCCTGGCCAGCTCAC 1140

Qy      1616 ACTCTTGTCCTGGGAGGGGCAGCCTGATCTCACCTCCACCTAGTACCTTGGGGACTGAGG 1675
Db      1139 ACTCTTGTCCTGGGAGGGGCAGCCTGATCTCACCTCCACCTAGTACCTTGGGGACTGAGG 1080

Qy      1676 ACCTTTTGGCTTCTCTGGAGCCTGCAAGCCTCTTCCCATGTGTCCAGCTGCTCTTCCTGC 1735
Db      1079 ACCTTTTGGCTTCTCTGGAGCCTGCAAGCCTCTTCCCATGTGTCCAGCTGCTCTTCCTGC 1020

Qy      1736 TACAAAGGGGACTGCTCACAGTGGCCTCAGCTTGGTGGTTTTGAGGGGCCGCCCCCCGGC 1795
Db      1019 TACAAAGGGGACTGCTCACAGTGGCCTCAGCTTGGTGGTTTTGAGGGGCCGCCCCCCGGC 960

Qy      1796 CCTCCATAAGGGTATCCTGGGCCTGAGAATTCTGCATCTGCCATTGGAGGATGGACAGCC 1855
Db       959 CCTCCATAAGGGTATCCTGGGCCTGAGAATTCTGCATCTGCCATTGGAGGATGGACAGCC 900

Qy      1856 TCAAATGGAAGGAGTCCCACGGGAGATGGGTCCGAGGTCCGGCTGTGGCCATCCAGCCCC 1915
Db       899 TCAAATGGAAGGAGTCCCACGGGAGATGGGTCCGAGGTCCGGCTGTGGCCATCCAGCCCC 840

Qy      1916 CTGTGGCTTGTCCAGCCTCTGTGCACCCCTGGTGTCTTCACTCCAGGGGCAGACAGCAGC 1975
Db       839 CTGTGGCTTGTCCAGCCTCTGTGCACCCCTGGTGTCTTCACTCCAGGGGCAGACAGCAGC 780

Qy      1976 CACTGCAGTTCCTTTCTTCGTGAGTAACAGTAGTGATAGCAGCTGGGGCTAACAGGCTAG 2035
Db       779 CACTGCAGTTCCTTTCTTCGTGAGTAACAGTAGTGATAGCAGCTGGGGCTAACAGGCTAG 720

Qy      2036 GCTTTGTGTTCTGCGCATTTGGTCAGCTTCTCACTCGATCCTCCCTAAAGCAATGGGGAG 2095
Db       719 GCTTTGTGTTCTGCGCATTTGGTCAGCTTCTCACTCGATCCTCCCTAAAGCAATGGGGAG 660

Qy      2096 GCCCCCACTAGCCCAGTTTTCAGGAAGTCAACTGGGAGGTTAGATGGGGGCCAGGGTCCC 2155
Db       659 GCCCCCACTAGCCCAGTTTTCAGGAAGTCAACTGGGAGGTTAGATGGGGGCCAGGGTCCC 600

Qy      2156 ACAGCTACTGATGGCCCGAGCCAGGTTGAGCTTCCTGGTGTCCAGTCCGGATCCCACTTG 2215
Db       599 ACAGCTACTGATGGCCCGAGCCAGGTTGAGCTTCCTGGTGTCCAGTCCGGATCCCACTTG 540

Qy      2216 CAGATCTCATGCTCTCAGATAGGTGGGACAAGTTCTTTTGTCACAGTGCTGGCTCTGTCC 2275
Db       539 CAGATCTCATGCTCTCAGATAGGTGGGACAAGTTCTTTTGTCACAGTGCTGGCTCTGTCC 480

Qy      2276 TGAGGCCTCATTGCTGGCTGGGTGTGCTCTGCTGGGAAAAGCTTTGCGGGGCTTGCTTGG 2335
Db       479 TGAGGCCTCATTGCTGGCTGGGTGTGCTCTGCTGGGAAAAGCTTTGCGGGGCTTGCTTGG 420

Qy      2336 TTAACCACAGAAGAGAAGGGGACTGTTTGGGGTGCCTCTCTGCAGCCTCCCCGTGCTGGG 2395
Db       419 TTAACCACAGAAGAGAAGGGGACTGTTTGGGGTGCCTCTCTGCAGCCTCCCCGTGCTGGG 360

Qy      2396 TGGAAGCACGGTTACTGTGTTCTCTAATGTTCATGTATTTAAAATGATTTCTTTCTAAAG 2455
Db       359 TGGAAGCACGGTTACTGTGTTCTCTAATGTTCATGTATTTAAAATGATTTCTTTCTAAAG 300

Qy      2456 ATGTAACCTCCACACCTTTCTCCAGATTGGGTGACTCTTTTCTAAAGGTGGTGGGAGTAT 2515
Db       299 ATGTAACCTCCACACCTTTCTCCAGATTGGGTGACTCTTTTCTAAAGGTGGTGGGAGTAT 240

Qy      2516 CTGTCGGGGTGGTGTGGCCCTTGGATGGGTCAGGTGGGTGTGAGAGGTCCTGGGGAGGTG 2575
Db       239 CTGTCGGGGTGGTGTGGCCCTTGGATGGGTCAGGTGGGTGTGAGAGGTCCTGGGGAGGTG 180

Qy      2576 GGCGTTGAGCTCAAAGTTGTCCTACTGCCATGTTTTTGTACCTGAAATAAAGCATATTTT 2635
Db       179 GGCGTTGAGCTCAAAGTTGTCCTACTGCCATGTTTTTGTACCTGAAATAAAGCATATTTT 120

Qy      2636 GCACTTGTTACTGTACCATAGTGCGGACGAGAAGTCTGTATGTGGGATCTGTGCTTGGGT 2695
Db       119 GCACTTGTTACTGTACCATAGTGCGGACGAGAAGTCTGTATGTGGGATCTGTGCTTGGGT 60

Qy      2696 TAGAATGCAAATAAAACTCACATTTGTAAGAAAAAAAAAAAAAAATAAAAAGATGCGGCC 2754
Db        59 TAGAATGCAAATAAAACTCACATTTGTAAGAAAAAAAAAAAAAATAAAAAGATGCGGCC 1
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```
RESULT 4
US-09-989-920-99
; Sequence 99, Application US/09989920
; Patent No. US20020172957A1
; GENERAL INFORMATION:
;  APPLICANT: Macina, Roberto
;  APPLICANT:  Recipon, Herve
;  APPLICANT:  Chen, Sei-Yu
;  APPLICANT:  Sun, Yongming
;  APPLICANT:  Liu, Chenghua
;  TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prot
;  FILE REFERENCE: DEX-0291
;  CURRENT APPLICATION NUMBER: US/09/989,920
;  CURRENT FILING DATE:  2001-11-21
;  PRIOR APPLICATION NUMBER: 60/252,500
;  PRIOR FILING DATE: 2000-11-22
;  NUMBER OF SEQ ID NOS: 284
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 99
;   LENGTH: 960
;   TYPE: DNA
;   ORGANISM: Homo sapien
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (716)..(716)
;   OTHER INFORMATION: a, c, g or t
US-09-989-920-99

  Query Match             22.2%;  Score 612.4;  DB 9;  Length 960;
  Best Local Similarity   99.4%;  Pred. No. 8.4e-157;
  Matches  646;  Conservative    0;  Mismatches    1;  Indels    3;  Gaps    3;

Qy       1658 GTACCTTGGGGACTGAGGACCTTTTGGCTTCTCTGGAGCCTGCAAGCCTCTTCCCATGTG 1717
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Db         41 GTACCTTGGGGACTGAGGACCTTTTGGCTTCTCTGGAGCCTGCAAGCCTCTTCCCATGTG 100

Qy       1718 TCCAGCTGCTCTTCCTGCTACAAAGGGGACTGCTCACAGTGGCCTCAGCTTGGTGGTTTT 1777
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        101 TCCAGCTGCTCTTCCTGCTACAAAGGGGACTGCTCACAGTGGCCTCAGCTTGGTGGTTTT 160

Qy       1778 GAGGGGCCGCCCCCCGGCCCTCCATAAGGGTATCCTGGGCCTGAGAATTCTGCATCTGCC 1837
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        161 GAGGGGCCGCCCCCCGGCCCTCCATAAGGGTATCCTGGGCCTGAGAATTCTGCATCTGCC 220

Qy       1838 ATTGGAGGATGGACAGCCTCAAATGGAAGGAGTCCCACGGGAGATGGGTCCGAGGTCCGG 1897
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        221 ATTGGAGGATGGACAGCCTCAAATGGAAGGAGTCCCACGGGAGATGGGTCCGAGGTCCGG 280

Qy       1898 CTGTGGCCATCCAGCCCCCTGTGGCTTGTCCAGCCTCTGTGCACCCCTGGTGTCTTCACT 1957
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 CTGTGGCCATCCAGCCCCCTGTGGCTTGTCCAGCCTCTGTGCACCCCTGGTGTCTTCACT 340

Qy       1958 CCAGGGGCAGACAGCAGCCACTGCAGTTCCTTTCTTCGTGAGTAACAGTAGTGATAGCAG 2017
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        341 CCAGGGGCAGACAGCAGCCACTGCAGTTCCTTTCTTCGTGAGTAACAGTAGTGATAGCAG 400

Qy       2018 CTGGGGCTAACAGGCTAGGCTTTGTGTTCTGCGCATTTGGTCAGCTTCTCACTCGATCCT 2077
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        401 CTGGGGCTAACAGGCTAGGCTTTGTGTTCTGCGCATTTGGTCAGCTTCTCACTCGATCCT 460

Qy       2078 CCCTAAAGCAATGGGGAGGCCCCCACTAGCCCAGTTTTCAGGAAGTCAACTGGGAGGTTA 2137
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        461 CCCTAAAGCAATGGGGAGGCCCCCACTAGCCCAGTTTTCAGGAAGTCAACTGGGAGGTTA 520

Qy       2138 GATGGGGGCCAGGGTCCCACA-GCTACTGATGGCCCGAGCCAGGTTGAGCTTCCTGGTGT 2196
             ||||||||||||||||||||| || ||||||||||||||||||||||||||||||||||||||||
Db        521 GATGGGGGCCAGGGTCCCACATGCTGCTGATGGCCCGAGCCAGGTTGAGCTTCCTGGTGT 580

Qy       2197 CCAGTCCGGAT-CCCACTTGCAGATCTCATGCTCTCAGATAGGTGGGACAAGTTCTTTTG 2255
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Db        581 CCAGTCCGGATCCCCACTTGCAGATCTCATGCTCTCAGATAGGTGGGACAAGTTCTTTTG 640

Qy       2256 TCACAGTGCTGG-CTCTGTCCTGAGGCCTCATTGCTGGCTGGGTGTGCTC 2304
             ||||||||||| |||||||||||||||||||||||||||||||||||||||
Db        641 TCACAGTGCTGGCCTCTGTCCTGAGGCCTCATTGCTGGCTGGGTGTGCTC 690


RESULT 5
US-10-172-118-2364/c
; Sequence 2364, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
;  APPLICANT: Dai, Hongyue
;  APPLICANT:  He, Yudong
;  APPLICANT:  Linsley, Peter
;  APPLICANT:  Mao, Mao
;  APPLICANT:  Roberts, Chris
;  APPLICANT:  Van 't Veer, Laura
;  APPLICANT:  Van de Vijver, Marc
;  APPLICANT:  Bernards, Rene
;  TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
;  FILE REFERENCE: 9301-175-999
;  CURRENT APPLICATION NUMBER: US/10/172,118
;  CURRENT FILING DATE:  2002-06-14
;  PRIOR APPLICATION NUMBER: 60/380,770
;  PRIOR FILING DATE: 2002-05-14
;  NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 2364
;   LENGTH: 524
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: Contig46362
;   DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-2364

  Query Match             19.0%;  Score 524;  DB 15;  Length 524;
  Best Local Similarity   100.0%;  Pred. No. 1e-132;
  Matches  524;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        488 TCCCCCAATCTATGGGTCACAGCTAACAGATCTGAGGGCAACTGCTGTGCTAGTGGCCAG 547
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        524 TCCCCCAATCTATGGGTCACAGCTAACAGATCTGAGGGCAACTGCTGTGCTAGTGGCCAG 465

Qy        548 GGCTGCACCTGCCATCCCCGGCTCTGCCACTTTAGGGCCTTCTAGAGGCAGTGTCCTTAG 607
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        464 GGCTGCACCTGCCATCCCCGGCTCTGCCACTTTAGGGCCTTCTAGAGGCAGTGTCCTTAG 405

Qy        608 GAAGTAGCTCTGAGGCATGGGTTTTCTGCTCCTGTGCAGGGCAGCTGATGGGATAAGGTG 667
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        404 GAAGTAGCTCTGAGGCATGGGTTTTCTGCTCCTGTGCAGGGCAGCTGATGGGATAAGGTG 345

Qy        668 GGGAAGGACGGTCAGTGCTTGGGCCCCAGCTGGCCAGCCTGGCGATGGGGAAACCAAACC 727
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Db        344 GGGAAGGACGGTCAGTGCTTGGGCCCCAGCTGGCCAGCCTGGCGATGGGGAAACCAAACC 285

Qy        728 ATGTCCCCCAGCGAAGGGCCAGAGTGGGAACCTGTCCTCATGCCCTTCGTCCTGAGGAGC 787
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        284 ATGTCCCCCAGCGAAGGGCCAGAGTGGGAACCTGTCCTCATGCCCTTCGTCCTGAGGAGC 225

Qy        788 CCTGAGGTGGGCAGCAGGGGCCAGGGGAAGTTTTCAGGCCTTCATCAAAGAGAACAACAT 847
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Db        224 CCTGAGGTGGGCAGCAGGGGCCAGGGGAAGTTTTCAGGCCTTCATCAAAGAGAACAACAT 165

Qy        848 CCTCAGCTCCGCACCCCTCATCCTGTATCAGCACTTACCGGTGTGTGACTGCCCTTGTCA 907
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        164 CCTCAGCTCCGCACCCCTCATCCTGTATCAGCACTTACCGGTGTGTGACTGCCCTTGTCA 105

Qy        908 GCTAGCATACGGTGGGCCCACCTGGCCCACTGGCTGTTTATGCCACTGATTTATGATAGG 967
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        104 GCTAGCATACGGTGGGCCCACCTGGCCCACTGGCTGTTTATGCCACTGATTTATGATAGG 45

Qy        968 GAATATTATCTTTGAACCCAATGAAGTGTTTTCTCCCCCATCAC 1011
              |||||||||||||||||||||||||||||||||||||||||||
Db         44 GAATATTATCTTTGAACCCAATGAAGTGTTTTCTCCCCCATCAC 1
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RESULT 6
US-10-342-887-2364/c
; Sequence 2364, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
;  APPLICANT: Dai, Hongyue
;  APPLICANT:  He, Yudong
;  APPLICANT:  Linsley, Peter S.
;  APPLICANT:  Mao, Mao
;  APPLICANT:  Roberts, Christopher J.
;  APPLICANT:  Van 't Veer, Laura Johanna
;  APPLICANT:  Van de Vijver, Marc J.
;  APPLICANT:  Bernards, Rene
;  TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
;  FILE REFERENCE: 9301-188-999
;  CURRENT APPLICATION NUMBER: US/10/342,887
;  CURRENT FILING DATE:  2003-01-15
;  PRIOR APPLICATION NUMBER: 60/298,918
;  PRIOR FILING DATE: 2001-06-18
;  PRIOR APPLICATION NUMBER: 60/380,710
;  PRIOR FILING DATE: 2002-05-14
;  PRIOR APPLICATION NUMBER: 10/172,118
;  PRIOR FILING DATE: 2002-06-14
;  NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 2364
;   LENGTH: 524
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-342-887-2364

  Query Match            19.0%;  Score 524;  DB 16;  Length 524;
  Best Local Similarity  100.0%;  Pred. No. 1e-132;
  Matches  524;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        488 TCCCCCAATCTATGGGTCACAGCTAACAGATCTGAGGGCAACTGCTGTGCTAGTGGCCAG 547
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        524 TCCCCCAATCTATGGGTCACAGCTAACAGATCTGAGGGCAACTGCTGTGCTAGTGGCCAG 465

Qy        548 GGCTGCACCTGCCATCCCCGGCTCTGCCACTTTAGGGCCTTCTAGAGGCAGTGTCCTTAG 607
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        464 GGCTGCACCTGCCATCCCCGGCTCTGCCACTTTAGGGCCTTCTAGAGGCAGTGTCCTTAG 405

Qy        608 GAAGTAGCTCTGAGGCATGGGTTTTCTGCTCCTGTGCAGGGCAGCTGATGGGATAAGGTG 667
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        404 GAAGTAGCTCTGAGGCATGGGTTTTCTGCTCCTGTGCAGGGCAGCTGATGGGATAAGGTG 345

Qy        668 GGGAAGGACGGTCAGTGCTTGGGCCCCAGCTGGCCAGCCTGGCGATGGGGAAACCAAACC 727
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        344 GGGAAGGACGGTCAGTGCTTGGGCCCCAGCTGGCCAGCCTGGCGATGGGGAAACCAAACC 285

Qy        728 ATGTCCCCCAGCGAAGGGCCAGAGTGGGAACCTGTCCTCATGCCCTTCGTCCTGAGGAGC 787
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        284 ATGTCCCCCAGCGAAGGGCCAGAGTGGGAACCTGTCCTCATGCCCTTCGTCCTGAGGAGC 225

Qy        788 CCTGAGGTGGGCAGCAGGGGCCAGGGGAAGTTTTCAGGCCTTCATCAAAGAGAACAACAT 847
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        224 CCTGAGGTGGGCAGCAGGGGCCAGGGGAAGTTTTCAGGCCTTCATCAAAGAGAACAACAT 165

Qy        848 CCTCAGCTCCGCACCCCTCATCCTGTATCAGCACTTACCGGTGTGTGACTGCCCTTGTCA 907
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        164 CCTCAGCTCCGCACCCCTCATCCTGTATCAGCACTTACCGGTGTGTGACTGCCCTTGTCA 105

Qy        908 GCTAGCATACGGTGGGCCCACCTGGCCCACTGGCTGTTTATGCCACTGATTTATGATAGG 967
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        104 GCTAGCATACGGTGGGCCCACCTGGCCCACTGGCTGTTTATGCCACTGATTTATGATAGG 45

Qy        968 GAATATTATCTTTGAACCCAATGAAGTGTTTTCTCCCCCATCAC 1011
              |||||||||||||||||||||||||||||||||||||||||||
Db         44 GAATATTATCTTTGAACCCAATGAAGTGTTTTCTCCCCCATCAC 1

RESULT 7
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US-10-074-475-1
; Sequence 1, Application US/10074475
; Publication No. US20030092898A1
; GENERAL INFORMATION:
;  APPLICANT: Salceda, Susana
;  APPLICANT:  Macina, Roberto
;  APPLICANT:  Hu, Ping
;  APPLICANT:  Recipon, Herve
;  APPLICANT:  Karra, Kalpana
;  APPLICANT:  Cafferkey, Robert
;  APPLICANT:  Sun, Yongming
;  APPLICANT:  Liu, Chenghua
;  TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific
;  TITLE OF INVENTION:  Genes and Proteins
;  FILE REFERENCE: DEX-0313
;  CURRENT APPLICATION NUMBER: US/10/074,475
;  CURRENT FILING DATE:  2002-02-13
;  PRIOR APPLICATION NUMBER: 60/268,292
;  PRIOR FILING DATE: 2001-02-13
;  NUMBER OF SEQ ID NOS: 295
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-074-475-1

  Query Match            17.6%;  Score 483.8;  DB 14;  Length 591;
  Best Local Similarity  97.5%;  Pred. No. 1.2e-121;
  Matches  555;  Conservative    0;  Mismatches    7;  Indels    7;  Gaps    6;

Qy       1735 CTACAAAGGGGACTGCTCACAGTGGCCTCAGCTTGGTGGTTTTGAGGGGCCGCCCCCCGG 1794
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         12 CTACAAAGGGGACTGCTCACAGTGGCCTCAGCTTGGTGGTTTTGAGGGGCCGCCCCCCGG 71

Qy       1795 CCCTCCATAAGGGTATCCTGGGCCTGAGAATTCTGCATCTGCCATTGGA-GGATGGACAG 1853
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||| ||||
Db         72 CCCTCCATAAGGGTATCCTGGGCCTGAGAATTCTGCATCTGCCATTGGATGGATGTACAG 131

Qy       1854 CCTCAAATGGAAG-GAGTCCCACGGGAGATGGGTCCGAGGTCC-GGCTGTGGCCATCCAG 1911
              ||||||||||||| |||||||||||||||||||||||||||| ||||||||||||||||
Db        132 CCTCAAATGGAAGTGAGTCCCACGGGAGATGGGTCCGAGGTCCAGGCTGTGGCCATCCAG 191

Qy       1912 CCCCCTGTGGCTTGTCCAGCCTCTGTGCACCCCTGGTGTCTTCACTCCAGGGGCAGACAG 1971
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        192 CCCCCTGTGGCTTGTCCAGCCTCTGTGCACCCCTGGTGTCTTCACTCCAGGGGCAGACAG 251

Qy       1972 CAGCCACTGCAGTTCCTTTCTTCGTGAG-TAACAGTAGTGATAGCAGCTGGGGCTAACAG 2030
              ||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db        252 TAGCCACTGCAGTTCCTTTCTTCGTGAGATAACAGTAGTGATAGCAGCTGGGGCTAACAG 311

Qy       2031 GCTAGGCTTTGTGTTCTGCGCATTTGGTCAGCTTCTCACTCGATCCTCCCTAAAGCAATG 2090
              ||||||||| |||| ||||||||||||||||||||||||||||||||||||||||||||
Db        312 GCTAGGCTTAGTGTCCTGCGCATTTGGTCAGCTTCTCACTCGATCCTCCCTAAAGCAATG 371

Qy       2091 GGGAGGCCCCCCACTAGCCCAGTTTTCAGGAAGTCAACTGGGAGGTTAGATGGGGGCCAG- 2149
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        372 GGGAGGCCCCCACTAGCCCAGTTTTCAGGAAGTCAACTGGGAGGTTAGATGGGGGCCAGA 431

Qy       2150 GGTCCCACAGCTACTGATGGCCCGAGCCAGGTTGAGCTT--CCTGGTGTCCAGTCCGGAT 2207
              |||||||||||||||||||||||||||||||||||||||  | | ||||||||||||||
Db        432 GGTCCCACAGCTACTGATGGCCCGAGCCAGGTTGAGCTTTCCTGGATGTCCAGTCCGGAT 491

Qy       2208 CCCACTTGCAGATCTCATGCTCTCAGATAGGTGGGACAAGTTCTTTTGTCACAGTGCTGG 2267
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        492 CCCACTTGCAGATCTCATGCTCTCAGATAGGTGGGACAAGTTCTTTTGTCACAGTGCTGG 551

Qy       2268 CTCTGTCCTGAGGCCTCATTGCTGGCTGG 2296
              |||||||||||||||||||||||||||||
Db        552 CTCTGTCCTGAGGCCTCATTGCTGGCTGG 580

RESULT 8
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```
US-10-609-021-176
  Sequence 176, Application US/10609021
  Publication No. US20040086913A1
  GENERAL INFORMATION:
   APPLICANT: Williams, Lewis T.
   APPLICANT:  Escobedo, Jaime
   APPLICANT:  Innis, Michael A.
   APPLICANT:  Garcia, Pablo Dominiguez
   APPLICANT:  Sudduth-Klinger, Julie
   APPLICANT:  Reinhard, Christoph
   APPLICANT:  He, Zhijun
   APPLICANT:  Randazzo, Filippo
   APPLICANT:  Kennedy, Giulia C.
   APPLICANT:  Pot, David
   APPLICANT:  Kassam, Altaf
   APPLICANT:  Lamson, George
   APPLICANT:  Drmanac, Radoje
   APPLICANT:  Dickson, Mark
   APPLICANT:  Labat, Ivan
   APPLICANT:  Jones, Lee William
   TITLE OF INVENTION: Human Genes and Gene Expression Products
   TITLE OF INVENTION:  XVI
   FILE REFERENCE: 2300-1625CON
   CURRENT APPLICATION NUMBER: US/10/609,021
   CURRENT FILING DATE:  2003-06-26
   PRIOR APPLICATION NUMBER: 60/192,583
   PRIOR FILING DATE: 2000-03-28
   PRIOR APPLICATION NUMBER: 09/819,150
   PRIOR FILING DATE: 2001-03-27
   NUMBER OF SEQ ID NOS: 324
   SOFTWARE: FastSEQ for Windows Version 4.0
  SEQ ID NO 176
    LENGTH: 395
    TYPE: DNA
    ORGANISM: Homo sapiens
US-10-609-021-176

   Query Match             13.0%;  Score 357.4;  DB 16;  Length 395;
   Best Local Similarity   96.9%;  Pred. No. 4.2e-87;
   Matches  375;  Conservative    0;  Mismatches   11;  Indels    1;  Gaps    1;

Qy       1216 CAGACCTCCATTACCTCCATCCCTGTTGGATTATTTAAAGAAAGCCTCAGACAGTAAGGG 1275
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db             9 CAGACCTCCATTACCTCCATCCCTGTTGGATTATTTAAAGAAAGCCTCAGACAGTAAGGG 68

Qy       1276 C-TTTTTTAAAAGAATAAAATGACTTGGTTTGCGCTTGGAAGCAGGGGAAGCATTCAGAT 1334
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            69 CTTTTTTTAAAAGAATAAAATGACTTGGTTTGCGCTTGGAAGCAGGGGAAGCATTCAGAT 128

Qy       1335 GAGCGGTTTCTGCATTAACCCTGCCTATCACGCATCTCGTGTCCTGTGTGGCTGGCGAGC 1394
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 GAGCGGTTTCTGCATTAACCCTGCCTATCACGCATCTCGTGTCCTGTGTGGCTGGCGAGC 188

Qy       1395 CCCCCTTGGAAGGTTCTGGTGCTTCAGCTGGCTCCTGCAGAGTCCACCCCGCCTCGTGGT 1454
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 CCCCCTTGGAAGGTTCTGGTGCTTCAGCTGGCTCCTGCAGAGTCCACCCCGCCTCGTGGT 248

Qy       1455 GGGAATGCAGAGCCCTTTGCTTTCCTTCTTGCCGCCTGCTTCCTGTTCCTGGGGACCCGC 1514
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 GGGAATGCAGAGCCCTTTGCTTTCCTTCTTGCCGCCTGCTTCCTGTTCCTGGGGACCCGC 308

Qy       1515 TGGGCCTTTGGTCTGCATCCCCTGGCCAGGTCCCTCAGGGTTGATGCGTGGAGAAGGACT 1574
             |||||||||||||||||||||||||||||||||||| ||||||| | |||||||||
Db        309 TGGGCCTTTGGTCTGCATCCCCTGGCCAGGTCCCTCAGGGCTGATGCGCGTAGAAGGACT 368

Qy       1575 TTGAGCAGTGGTGGGCAGCAGTGGCCT 1601
             |||||||||||||       || |||
Db        369 TTGAGCAGTGGTGGCAGCACTTGCCCT 395


RESULT 9
US-10-116-712-429
  Sequence 429, Application US/10116712
; Publication No. US20030194764A1
; GENERAL INFORMATION:
;  APPLICANT: Bangur, Chaitanya S.
;  APPLICANT:  Switzer, Ann
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 210121.568
;  CURRENT APPLICATION NUMBER: US/10/116,712
;  CURRENT FILING DATE:  2002-04-07
;  NUMBER OF SEQ ID NOS: 670
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 429
;   LENGTH: 295
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-116-712-429

  Query Match             10.7%;  Score 295;  DB 15;  Length 295;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-70;
  Matches  295;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1723 CTGCTCTTCCTGCTACAAAGGGGACTGCTCACAGTGGCCTCAGCTTGGTGGTTTTGAGGG 1782
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CTGCTCTTCCTGCTACAAAGGGGACTGCTCACAGTGGCCTCAGCTTGGTGGTTTTGAGGG 60

Qy       1783 GCCGCCCCCCCGGCCCTCCATAAGGGTATCCTGGGCCTGAGAATTCTGCATCTGCCATTGG 1842
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCGCCCCCCCGGCCCTCCATAAGGGTATCCTGGGCCTGAGAATTCTGCATCTGCCATTGG 120

Qy       1843 AGGATGGACAGCCTCAAATGGAAGGAGTCCCACGGGAGATGGGTCCGAGGTCCGGCTGTG 1902
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AGGATGGACAGCCTCAAATGGAAGGAGTCCCACGGGAGATGGGTCCGAGGTCCGGCTGTG 180

Qy       1903 GCCATCCAGCCCCCTGTGGCTTGTCCAGCCTCTGTGCACCCCTGGTGTCTTCACTCCAGG 1962
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCATCCAGCCCCCTGTGGCTTGTCCAGCCTCTGTGCACCCCTGGTGTCTTCACTCCAGG 240

Qy       1963 GGCAGACAGCAGCCACTGCAGTTCCTTTCTTCGTGAGTAACAGTAGTGATAGCAG 2017
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GGCAGACAGCAGCCACTGCAGTTCCTTTCTTCGTGAGTAACAGTAGTGATAGCAG 295


RESULT 10
US-09-989-920-90/c
; Sequence 90, Application US/09989920
; Patent No. US20020172957A1
; GENERAL INFORMATION:
;  APPLICANT: Macina, Roberto
;  APPLICANT:  Recipon, Herve
;  APPLICANT:  Chen, Sei-Yu
;  APPLICANT:  Sun, Yongming
;  APPLICANT:  Liu, Chenghua
;  TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Proteins
;  FILE REFERENCE: DEX-0291
;  CURRENT APPLICATION NUMBER: US/09/989,920
;  CURRENT FILING DATE:  2001-11-21
;  PRIOR APPLICATION NUMBER: 60/252,500
;  PRIOR FILING DATE: 2000-11-22
;  NUMBER OF SEQ ID NOS: 284
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 90
;   LENGTH: 251
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-989-920-90

  Query Match             8.1%;  Score 224.4;  DB 9;  Length 251;
  Best Local Similarity   98.8%;  Pred. No. 9.6e-51;
  Matches  237;  Conservative    0;  Mismatches    1;  Indels    2;  Gaps    1;

Qy       2381 CCTCCCCGTGCTGGGTGGAAGCACGGTTACTGTGTTCTCTAATGTTCATGTATTTAAAAT 2440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 CCTCCCCGTGCTGGGTGGAAGCACGGTTACTGTGTTCTCTAATGTTCATGTATTTAAAAT 192
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Qy       2441 GATTTCTTTCTAAAGATGTAACCTCCACACCTTTCTCCAGATTGGGTGACTCTTTTCTAA 2500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        191 GATTTCTTTCTAAAGATGTAACCTCCACACCTTTCTCCAGATTGGGTGACTCTTTTCTAA 132

Qy       2501 AGGTGGTGGGAGTATCTGTCGGGGTGGTGTGGCCCTTGGATGGGTCAGGTGGGTGTGAGA 2560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        131 AGGTGGTGGGAGTATCTGTCGGGGTGGTGTGGCCCTTGGATGGGTCAGGTGGGTGTGAGA 72

Qy       2561 GGTCCTGGGGAGGT--GGGCGTTGAGCTCAAAGTTGTCCTACTGCCATGTTTTTGTACCT 2618
             |||||||||||||  | ||||||||||||||||||||||||||||||||||||||||||
Db          71 GGTCCTGGGGAGGTGCGCGCGTTGAGCTCAAAGTTGTCCTACTGCCATGTTTTTGTACCT 12


RESULT 11
US-10-102-524-1276/c
; Sequence 1276, Application US/10102524
; Publication No. US20030109434A1
; GENERAL INFORMATION:
;  APPLICANT: Algate, Paul A.
;  APPLICANT:  Mannion, Jane
;  APPLICANT:  Gaiger, Alexander
;  APPLICANT:  Gordon, Brian
;  APPLICANT:  Harlocker, Susan L.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
;  TITLE OF INVENTION:  THERAPY AND DIAGNOSIS OF KIDNEY CANCER
;  FILE REFERENCE: 210121.572
;  CURRENT APPLICATION NUMBER: US/10/102,524
;  CURRENT FILING DATE:  2002-03-19
;  NUMBER OF SEQ ID NOS: 1863
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1276
;   LENGTH: 161
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-102-524-1276

  Query Match             5.8%;  Score 161;  DB 15;  Length 161;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-33;
  Matches  161;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1727 TCTTCCTGCTACAAAGGGGACTGCTCACAGTGGCCTCAGCTTGGTGGTTTTGAGGGGCCG 1786
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        161 TCTTCCTGCTACAAAGGGGACTGCTCACAGTGGCCTCAGCTTGGTGGTTTTGAGGGGCCG 102

Qy       1787 CCCCCCGGCCCTCCATAAGGGTATCCTGGGCCTGAGAATTCTGCATCTGCCATTGGAGGA 1846
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        101 CCCCCCGGCCCTCCATAAGGGTATCCTGGGCCTGAGAATTCTGCATCTGCCATTGGAGGA 42

Qy       1847 TGGACAGCCTCAAATGGAAGGAGTCCCACGGGAGATGGGTC 1887
             |||||||||||||||||||||||||||||||||||||||||
Db          41 TGGACAGCCTCAAATGGAAGGAGTCCCACGGGAGATGGGTC 1


RESULT 12
US-09-854-867-10
; Sequence 10, Application US/09854867
; Publication No. US20030224356A1
; GENERAL INFORMATION:
;  APPLICANT: JOAN, KNOLL H
;  APPLICANT:  ROGAN, PETER K
;  TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING
;  FILE REFERENCE: 30307
;  CURRENT APPLICATION NUMBER: US/09/854,867
;  CURRENT FILING DATE:  2003-05-08
;  NUMBER OF SEQ ID NOS: 613
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
;   LENGTH: 2285
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: repeat_region
;   LOCATION: (1)..(2285)
;   OTHER INFORMATION: cheshire
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (377)..(377)
;   OTHER INFORMATION: n is a, c, g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (580)..(580)
;   OTHER INFORMATION: n is a, c, g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (651)..(651)
;   OTHER INFORMATION: n is a, c, g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (664)..(664)
;   OTHER INFORMATION: n is a, c, g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (725)..(725)
;   OTHER INFORMATION: n is a, c, g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (728)..(728)
;   OTHER INFORMATION: n is a, c, g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1095)..(1095)
;   OTHER INFORMATION: n is a, c, g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1151)..(1151)
;   OTHER INFORMATION: n is a, c, g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1281)..(1281)
;   OTHER INFORMATION: n is a, c, g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1351)..(1351)
;   OTHER INFORMATION: n is a, c, g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1370)..(1370)
;   OTHER INFORMATION: n is a, c, g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1385)..(1385)
;   OTHER INFORMATION: n is a, c, g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1885)..(1885)
;   OTHER INFORMATION: n is a, c, g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1912)..(1912)
;   OTHER INFORMATION: n is a, c, g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1990)..(1990)
;   OTHER INFORMATION: n is a, c, g or t
US-09-854-867-10

  Query Match             3.4%;  Score 93.6;  DB 10;  Length 2285;
  Best Local Similarity   67.3%;  Pred. No. 2.5e-14;
  Matches  183;  Conservative    1;  Mismatches   70;  Indels   18;  Gaps    3;

Qy        957 TTTATGATAGGGAATATTATCTTTGAACCCAATGAAGTGTTTTCTCCCCCATCACAAAAA 1016
              || |||||||||| | || |||||||||| |   |           |   | ||| |
Db       2016 TTGATGATAGGGAACACTAACTTTGAACCCCAATTAAGCAAAATGTTATCCCWAAAAAGA 2075

Qy       1017 AAAAAATTCTTATTTTTAGTAGACATGTATTTACCAAAAATATGTACTCAATTATTGTAT 1076
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Db       2076 ATTCCATTCTTCTCATTAGTAGACCTGTATTA--CAAAAAATTGTACTCAATTATTATTW 2133

Qy       1077 TTTGGATTTTATCAATT-------TAAAAATTGTGGAAATTTGTTTGCTCTTA------- 1122

Db       2134 TTATTATATTTGAATTTCATCAATAAAAATTGTGGAATTTTTCTCTTGTTATATAAGT 2193

Qy       1123 --CGCCAACATAATATTGATTTTGCCTCTTGGCTCTGAAAGCCCAAAATATTTACCGTCT 1180

Db       2194 ACCTACATAATATCCTTGATTTTGCCTCTTGGCCCGCAAAGCCTAAAATATTTACTATCT 2253

Qy       1181 AGCCCGTTACAGAAAAAGTCTGCTGACTACTG 1212

Db       2254 GGCCCTTTACAGAAAAAGTTTGCCGACCCCTG 2285
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RESULT 13
US-09-764-878-292/c
; Sequence 292, Application US/09764878
; Patent No. US20020090615A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA121
; CURRENT APPLICATION NUMBER: US/09/764,878
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 292
; LENGTH: 32038
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-878-292

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  Query Match             2.7%;  Score 75;  DB 9;  Length 32038;
  Best Local Similarity   65.9%;  Pred. No. 1.5e-08;
  Matches  147;  Conservative    0;  Mismatches   60;  Indels   16;  Gaps    2;

Qy       1013 AAAAAAAAAATTCTTATTTTTAGTAGACATGTATTTACCAAAAATATGTACTCAATTATT 1072

Db      28877 AAATATTTAATTCTTTTCATTAGTAAACCCGTATTACAAAAAAAATTGTTCTAAATTATT 28818

Qy       1073 GTATTTTGGATTTTATCAATTTAAAAATTGTGGAAATTTGTTTGCTCTTACGC------- 1125

Db      28817 G--TTTTGAATTTTGTCAATAAAATTTTCGTGCAAATTTTATTTCTCTCTAGTTATTTAA 28760

Qy       1126 -------CAACATAATATTGATTTTGCCTCTTGGCTCTGAAAGCCCAAAATATTTACCGT 1178

Db      28759 GTATCTACATAACAATCTCAGTTTTACCTCTTAGCCCACAAAGCCTAAAATATTTACTAT 28700

Qy       1179 CTAGCCCGTTACAGAAAAAGTCTGCTGACTACTGAGCCAGACC 1221

Db      28699 CTGGCCCTTTATAGAAAAAGTTTCCTGACCTCTGCCCTAGAGC 28657
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RESULT 14
US-10-079-854-292/c
; Sequence 292, Application US/10079854
; Publication No. US20030054368A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA121C1
; CURRENT APPLICATION NUMBER: US/10/079,854
; CURRENT FILING DATE: 2002-02-22
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 292
; LENGTH: 32038
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-079-854-292

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  Query Match             2.7%;  Score 75;  DB 14;  Length 32038;
  Best Local Similarity   65.9%;  Pred. No. 1.5e-08;
  Matches  147;  Conservative    0;  Mismatches   60;  Indels   16;  Gaps    2;

Qy       1013 AAAAAAAAAATTCTTATTTTTAGTAGACATGTATTTACCAAAAATATGTACTCAATTATT 1072

Db      28877 AAATATTTAATTCTTTTCATTAGTAAACCCGTATTACAAAAAAAATTGTTCTAAATTATT 28818

Qy       1073 GTATTTTGGATTTTATCAATTTAAAAATTGTGGAAATTTGTTTGCTCTTACGC------- 1125

Db      28817 G--TTTTGAATTTTGTCAATAAAATTTTCGTGCAAATTTTATTTCTCTCTAGTTATTTAA 28760

Qy       1126 -------CAACATAATATTGATTTTGCCTCTTGGCTCTGAAAGCCCAAAATATTTACCGT 1178

Db      28759 GTATCTACATAACAATCTCAGTTTTACCTCTTAGCCCACAAAGCCTAAAATATTTACTAT 28700

Qy       1179 CTAGCCCGTTACAGAAAAAGTCTGCTGACTACTGAGCCAGACC 1221

Db      28699 CTGGCCCTTTATAGAAAAAGTTTCCTGACCTCTGCCCTAGAGC 28657
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RESULT 15
US-09-984-429-498
; Sequence 498, Application US/09984429
; Publication No. US20040010132A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 53 Human Secreted Proteins
; FILE REFERENCE: PZ018P2
; CURRENT APPLICATION NUMBER: US/09/984,429
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/244,591
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/288,143
; PRIOR FILING DATE: 1999-04-08
; PRIOR APPLICATION NUMBER: PCT/US98/21142
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/061,463
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,529
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/071,498
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,527
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,536
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,532
; PRIOR FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 727
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 498
; LENGTH: 32844
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-984-429-498

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  Query Match             2.7%;  Score 75;  DB 11;  Length 32844;
  Best Local Similarity   65.9%;  Pred. No. 1.5e-08;
  Matches  147;  Conservative    0;  Mismatches   60;  Indels   16;  Gaps    2;

Qy       1013 AAAAAAAAAATTCTTATTTTTAGTAGACATGTATTTACCAAAAATATGTACTCAATTATT 1072

Db       3968 AAATATTTAATTCTTTTCATTAGTAAACCCGTATTACAAAAAAAATTGTTCTAAATTATT 4027

Qy       1073 GTATTTTGGATTTTATCAATTTAAAAATTGTGGAAATTTGTTTGCTCTTACGC------- 1125

Db       4028 G--TTTTGAATTTTGTCAATAAAATTTTCGTGCAAATTTTATTTCTCTCTAGTTATTTAA 4085

Qy       1126 -------CAACATAATATTGATTTTGCCTCTTGGCTCTGAAAGCCCAAAATATTTACCGT 1178
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Db       4086 GTATCTACATAACAATCTCAGTTTTACCTCTTAGCCCACAAAGCCTAAAATATTTACTAT 4145

Qy       1179 CTAGCCCGTTACAGAAAAAGTCTGCTGACTACTGAGCCAGACC 1221
              || |||| ||| |||||||||| | |||||  |||  | ||| |
Db       4146 CTGGCCCTTTATAGAAAAAGTTTCCTGACCTCTGCCCTAGAGC 4188

Search completed: November 29, 2004, 15:19:46
Job time : 2343 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: November 29, 2004, 08:42:07 ; Search time 1281 Seconds
(without alignments)
11285.641 Million cell updates/sec

Title: US-09-989-920-100
Perfect score: 2754
Sequence: 1 gccagaagcagcctcagctt.....aaaaataaaaagatgcggcc 2754

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	2754	100.0	2754	6	ABX92058	Abx92058 Lung spec
	2	2754	100.0	2754	6	ABT07523	Abt07523 Human bre
c	3	2397.4	87.1	2399	6	ABX92049	Abx92049 Lung spec
	4	612.4	22.2	960	6	ABX92057	Abx92057 Lung spec
	5	554	20.1	611	5	ABV54530	Abv54530 Human pro
	6	483.8	17.6	591	6	ABT07522	Abt07522 Human bre
	7	357.4	13.0	395	4	AAS59058	Aas59058 Human can
	8	295	10.7	295	10	ADD49697	Add49697 Human lun
c	9	224.4	8.1	251	6	ABX92048	Abx92048 Lung spec
	10	76.6	2.8	736	3	AAZ35057	Aaz35057 Pluripote
c	11	75	2.7	32038	4	AAK90877	Aak90877 Human dig
c	12	75	2.7	32038	4	AAK89980	Aak89980 Human dig
c	13	75	2.7	32038	5	AAS30028	Aas30028 Human lun
c	14	75	2.7	32038	10	ADB33365	Adb33365 Human nov
	15	75	2.7	32844	12	ADJ12644	Adj12644 DNA fragm
	16	70.8	2.6	10410	12	ADN37124	Adn37124 DNA seque
	17	64.8	2.4	4153	4	AAK66121	Aak66121 Human imm
	18	58.8	2.1	120670	12	ADQ59167	Adq59167 MSI-H car
	19	56.6	2.1	2000	8	ADA71938	Ada71938 Rice gene
c	20	56.2	2.0	10472	12	ADJ12647	Adj12647 DNA fragm
c	21	56.2	2.0	240823	10	ADD69391	Add69391 Human PG-
c	22	56.2	2.0	240825	4	AAF24497	Aaf24497 Human PG-
c	23	56.2	2.0	240825	6	ABQ81802	Abq81802 Human PG-
c	24	55.8	2.0	147419	6	ABK83574	Abk83574 Human cDN
c	25	55	2.0	200620	12	ADO56277	Ado56277 Human pre
c	26	51.4	1.9	75033	12	ADP66763	Adp66763 Human end
c	27	50.8	1.8	1940	10	ADA52599	Ada52599 Human cod
c	28	50.8	1.8	2193	8	ABX05077	Abx05077 Human nov
c	29	50.8	1.8	2337	6	AAL49931	Aal49931 Human mol
	30	50.6	1.8	9544	4	AAL04799	Aal04799 Human rep
	31	50.6	1.8	9544	4	ABL97693	Abl97693 Human tes
	32	50.6	1.8	32476	4	AAK85314	Aak85314 Human imm
c	33	50.2	1.8	2000	8	ADA71938	Ada71938 Rice gene
	34	49.4	1.8	495	6	ABN79060	Abn79060 Human ORF
	35	49	1.8	3365	11	ADM02732	Adm02732 Human cDN
	36	49	1.8	6330	4	AAA54431	Aaa54431 11-cis re
	37	49	1.8	6330	10	ADD71027	Add71027 Human ret
	38	49	1.8	6330	12	ADQ19466	Adq19466 Human sof
	39	49	1.8	19806	6	ABN89476	Abn89476 Human deh
	40	47.4	1.7	14024	4	AAS36381	Aas36381 Human car
c	41	47.4	1.7	14024	5	AAS30157	Aas30157 Human lun
c	42	47.4	1.7	14024	10	ADB33494	Adb33494 Human nov
	43	47.4	1.7	14024	10	ADE47075	Ade47075 Human car
	44	47.4	1.7	28965	10	ADC86716	Adc86716 Human GPC
	45	47	1.7	265	3	AAC23203	Aac23203 Human sec

ALIGNMENTS

RESULT 1
ABX92058
ID ABX92058 standard; cDNA; 2754 BP.
XX
AC ABX92058;
XX
DT 08-MAY-2003 (first entry)
XX
DE Lung specific nucleic acid (LSNA) #100.
XX
KW Human; gene therapy; vaccine; lung specific antigen; cancer diagnosis;
KW cancer monitoring; cancer staging; cancer imaging; lung cancer;
KW non-cancerous diseases of the lung; transgenic animal; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200268633-A2.
XX
PD 06-SEP-2002.
XX
PF 21-NOV-2001; 2001WO-US043612.
XX
PR 22-NOV-2000; 2000US-0252500P.
XX
PA (DIAD-) DIADEXUS INC.
XX
PI Macina RA, Recipon H, Chen S, Sun Y, Liu C;
XX
DR WPI; 2002-713376/77.
XX
PT New isolated human nucleic acid molecule and polypeptide, useful for
PT identifying, diagnosing, monitoring, staging, imaging and treating lung
PT cancer and non-cancerous diseases of the lung.
XX
PS Claim 1; Page 246-248; 389pp; English.
XX
CC The invention describes an isolated human nucleic acid (I) encoding any
CC of 120 10-1533 residue amino acid sequences (S1), given in the
CC specification, comprising any of 164 179-12421 base pair sequences (S2),
CC given in the specification. The methods and compositions of the present
CC invention are useful for identifying, diagnosing, monitoring, staging,
CC imaging and treating lung cancer and non-cancerous diseases of the lung.
CC They are also used for identifying lung tissue, monitoring and
CC identifying and/or designing antagonists of the polypeptide of the

CC invention, gene therapy, production of transgenic animals and production
CC of engineered lung tissue for treatment and research. This sequence
CC encodes a lung specific nucleic acid
XX
SQ Sequence 2754 BP; 557 A; 720 C; 753 G; 724 T; 0 U; 0 Other;

Query Match 100.0%; Score 2754; DB 6; Length 2754;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2754; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GCCAGAAGCAGCCTCAGCTTGGCAAGGTGTGGAGATGACTGCTGTTCCCTTCGCATTTGG 60
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Db          1 GCCAGAAGCAGCCTCAGCTTGGCAAGGTGTGGAGATGACTGCTGTTCCCTTCGCATTTGG 60

Qy         61 GGAAAACAGGCTCCCTCGGTAGCTCGATGATCCTCTTTTGATCTTGTGTGACCTCCTGGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAAAACAGGCTCCCTCGGTAGCTCGATGATCCTCTTTTGATCTTGTGTGACCTCCTGGA 120

Qy        121 GAGTGGATGACGCTGGTGGCCTTAGCTTTTCTAGACAGTGTAAATTGCACTGGGCGATGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GAGTGGATGACGCTGGTGGCCTTAGCTTTTCTAGACAGTGTAAATTGCACTGGGCGATGT 180

Qy        181 CCCCAGAGCAGGGCAAGGTCTCTAGAGCGGGTCTCCCACATGACTGGCTTCACACAGGCA 240
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Db        181 CCCCAGAGCAGGGCAAGGTCTCTAGAGCGGGTCTCCCACATGACTGGCTTCACACAGGCA 240

Qy        241 CTTCCGCTCGGGTTGCATGCTCTGTGTCATCTTACCGGTCCAGGGTTGCAGGTAGGAAAT 300
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Db        241 CTTCCGCTCGGGTTGCATGCTCTGTGTCATCTTACCGGTCCAGGGTTGCAGGTAGGAAAT 300

Qy        301 GTTTGTACCCTCTTCTGATTGCCACCTCCTTCCCATCGCCCCTTAGGGACAGGGCTTGAG 360
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Db        301 GTTTGTACCCTCTTCTGATTGCCACCTCCTTCCCATCGCCCCTTAGGGACAGGGCTTGAG 360

Qy        361 GGCCAGTGAGGCGCTGGTCAGGCACCCCAGGCCTCCTTGGGACCTGCCCAGGGGCACCCT 420
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Db        361 GGCCAGTGAGGCGCTGGTCAGGCACCCCAGGCCTCCTTGGGACCTGCCCAGGGGCACCCT 420

Qy        421 GAGAGCTCCTGAAACCCCCACTTAGCTTCCAGACCTTTCTGCAAAAGCTCCTCCTGGCTT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GAGAGCTCCTGAAACCCCCACTTAGCTTCCAGACCTTTCTGCAAAAGCTCCTCCTGGCTT 480

Qy        481 TCCTCCCTCCCCCAATCTATGGGTCACAGCTAACAGATCTGAGGGCAACTGCTGTGCTAG 540
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Db        481 TCCTCCCTCCCCCAATCTATGGGTCACAGCTAACAGATCTGAGGGCAACTGCTGTGCTAG 540

Qy        541 TGGCCAGGGCTGCACCTGCCATCCCCGGCTCTGCCACTTTAGGGCCTTCTAGAGGCAGTG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TGGCCAGGGCTGCACCTGCCATCCCCGGCTCTGCCACTTTAGGGCCTTCTAGAGGCAGTG 600

Qy        601 TCCTTAGGAAGTAGCTCTGAGGCATGGGTTTTCTGCTCCTGTGCAGGGCAGCTGATGGGA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TCCTTAGGAAGTAGCTCTGAGGCATGGGTTTTCTGCTCCTGTGCAGGGCAGCTGATGGGA 660

Qy        661 TAAGGTGGGGAAGGACGGTCAGTGCTTGGGCCCCAGCTGGCCAGCCTGGCGATGGGGAAA 720
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Db        661 TAAGGTGGGGAAGGACGGTCAGTGCTTGGGCCCCAGCTGGCCAGCCTGGCGATGGGGAAA 720

Qy        721 CCAAACCATGTCCCCCAGCGAAGGGCCAGAGTGGGAACCTGTCCTCATGCCCTTCGTCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CCAAACCATGTCCCCCAGCGAAGGGCCAGAGTGGGAACCTGTCCTCATGCCCTTCGTCCT 780

Qy        781 GAGGAGCCCTGAGGTGGGCAGCAGGGGCCAGGGGAAGTTTTCAGGCCTTCATCAAAGAGA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GAGGAGCCCTGAGGTGGGCAGCAGGGGCCAGGGGAAGTTTTCAGGCCTTCATCAAAGAGA 840

Qy        841 ACAACATCCTCAGCTCCGCACCCCTCATCCTGTATCAGCACTTACCGGTGTGTGACTGCC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ACAACATCCTCAGCTCCGCACCCCTCATCCTGTATCAGCACTTACCGGTGTGTGACTGCC 900

Qy        901 CTTGTCAGCTAGCATACGGTGGGCCCACCTGGCCCACTGGCTGTTTATGCCACTGATTTA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CTTGTCAGCTAGCATACGGTGGGCCCACCTGGCCCACTGGCTGTTTATGCCACTGATTTA 960

Qy        961 TGATAGGGAATATTATCTTTGAACCCAATGAAGTGTTTTCTCCCCCATCACAAAAAAAAAA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TGATAGGGAATATTATCTTTGAACCCAATGAAGTGTTTTCTCCCCCATCACAAAAAAAAAA 1020

Qy       1021 AATTCTTATTTTTAGTAGACATGTATTTACCAAAAATATGTACTCAATTATTGTATTTTG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AATTCTTATTTTTAGTAGACATGTATTTACCAAAAATATGTACTCAATTATTGTATTTTG 1080

Qy       1081 GATTTTATCAATTTAAAAATTGTGGAAATTTGTTTGCTCTTACGCCAACATAATATTGAT 1140
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Db       1081 GATTTTATCAATTTAAAAATTGTGGAAATTTGTTTGCTCTTACGCCAACATAATATTGAT 1140

Qy       1141 TTTGCCTCTTGGCTCTGAAAGCCCAAAATATTTACCGTCTAGCCCGTTACAGAAAAAGTC 1200
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Db       1141 TTTGCCTCTTGGCTCTGAAAGCCCAAAATATTTACCGTCTAGCCCGTTACAGAAAAAGTC 1200

Qy       1201 TGCTGACTACTGAGCCAGACCTCCATTACCTCCATCCCTGTTGGATTATTTAAAGAAAGC 1260
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Db       1201 TGCTGACTACTGAGCCAGACCTCCATTACCTCCATCCCTGTTGGATTATTTAAAGAAAGC 1260

Qy       1261 CTCAGACAGTAAGGGCTTTTTTAAAAGAATAAAATGACTTGGTTTGCGCTTGGAAGCAGG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CTCAGACAGTAAGGGCTTTTTTAAAAGAATAAAATGACTTGGTTTGCGCTTGGAAGCAGG 1320

Qy       1321 GGAAGCATTCAGATGAGCGGTTTCTGCATTAACCCTGCCTATCACGCATCTCGTGTCCTG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GGAAGCATTCAGATGAGCGGTTTCTGCATTAACCCTGCCTATCACGCATCTCGTGTCCTG 1380

Qy       1381 TGTGGCTGGCGAGCCCCCCCTTGGAAGGTTCTGGTGCTTCAGCTGGCTCCTGCAGAGTCCA 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TGTGGCTGGCGAGCCCCCCTTGGAAGGTTCTGGTGCTTCAGCTGGCTCCTGCAGAGTCCA 1440

Qy       1441 CCCCGCCTCGTGGTGGGAATGCAGAGCCCTTTGCTTTCCTTCTTGCCGCCTGCTTCCTGT 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CCCCGCCTCGTGGTGGGAATGCAGAGCCCTTTGCTTTCCTTCTTGCCGCCTGCTTCCTGT 1500

Qy       1501 TCCTGGGGACCCGCTGGGCCTTTGGTCTGCATCCCCTGGCCAGGTCCCTCAGGGTTGATG 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 TCCTGGGGACCCGCTGGGCCTTTGGTCTGCATCCCCTGGCCAGGTCCCTCAGGGTTGATG 1560

Qy       1561 CGTGGAGAAGGACTTTGAGCAGTGGTGGGCAGCAGTGGCCTCCTGGCCAGCTCACACTCT 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 CGTGGAGAAGGACTTTGAGCAGTGGTGGGCAGCAGTGGCCTCCTGGCCAGCTCACACTCT 1620

Qy       1621 TGTCCTGGGAGGGGCAGCCTGATCTCACCTCCACCTAGTACCTTGGGGACTGAGGACCTT 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 TGTCCTGGGAGGGGCAGCCTGATCTCACCTCCACCTAGTACCTTGGGGACTGAGGACCTT 1680

Qy       1681 TTGGCTTCTCTGGAGCCTGCAAGCCTCTTCCCATGTGTCCAGCTGCTCTTCCTGCTACAA 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 TTGGCTTCTCTGGAGCCTGCAAGCCTCTTCCCATGTGTCCAGCTGCTCTTCCTGCTACAA 1740

Qy       1741 AGGGGACTGCTCACAGTGGCCTCAGCTTGGTGGTTTTGAGGGGCCGCCCCCCGGCCCTCC 1800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 AGGGGACTGCTCACAGTGGCCTCAGCTTGGTGGTTTTGAGGGGCCGCCCCCCGGCCCTCC 1800

Qy       1801 ATAAGGGTATCCTGGGCCTGAGAATTCTGCATCTGCCATTGGAGGATGGACAGCCTCAAA 1860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 ATAAGGGTATCCTGGGCCTGAGAATTCTGCATCTGCCATTGGAGGATGGACAGCCTCAAA 1860

Qy       1861 TGGAAGGAGTCCCACGGGAGATGGGTCCGAGGTCCGGCTGTGGCCATCCAGCCCCCTGTG 1920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 TGGAAGGAGTCCCACGGGAGATGGGTCCGAGGTCCGGCTGTGGCCATCCAGCCCCCTGTG 1920

Qy       1921 GCTTGTCCAGCCTCTGTGCACCCCTGGTGTCTTCACTCCAGGGGCAGACAGCAGCCACTG 1980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 GCTTGTCCAGCCTCTGTGCACCCCTGGTGTCTTCACTCCAGGGGCAGACAGCAGCCACTG 1980

Qy       1981 CAGTTCCTTTCTTCGTGAGTAACAGTAGTGATAGCAGCTGGGGCTAACAGGCTAGGCTTT 2040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 CAGTTCCTTTCTTCGTGAGTAACAGTAGTGATAGCAGCTGGGGCTAACAGGCTAGGCTTT 2040
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Qy       2041 GTGTTCTGCGCATTTGGTCAGCTTCTCACTCGATCCTCCCTAAAGCAATGGGGAGGCCCC 2100
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Db       2041 GTGTTCTGCGCATTTGGTCAGCTTCTCACTCGATCCTCCCTAAAGCAATGGGGAGGCCCC 2100

Qy       2101 CACTAGCCCAGTTTTCAGGAAGTCAACTGGGAGGTTAGATGGGGGCCAGGGTCCCACAGC 2160
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Db       2101 CACTAGCCCAGTTTTCAGGAAGTCAACTGGGAGGTTAGATGGGGGCCAGGGTCCCACAGC 2160

Qy       2161 TACTGATGGCCCGAGCCAGGTTGAGCTTCCTGGTGTCCAGTCCGGATCCCACTTGCAGAT 2220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 TACTGATGGCCCGAGCCAGGTTGAGCTTCCTGGTGTCCAGTCCGGATCCCACTTGCAGAT 2220

Qy       2221 CTCATGCTCTCAGATAGGTGGGACAAGTTCTTTTGTCACAGTGCTGGCTCTGTCCTGAGG 2280
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Db       2221 CTCATGCTCTCAGATAGGTGGGACAAGTTCTTTTGTCACAGTGCTGGCTCTGTCCTGAGG 2280

Qy       2281 CCTCATTGCTGGCTGGGTGTGCTCTGCTGGGAAAAGCTTTGCGGGGCTTGCTTGGTTAAC 2340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 CCTCATTGCTGGCTGGGTGTGCTCTGCTGGGAAAAGCTTTGCGGGGCTTGCTTGGTTAAC 2340

Qy       2341 CACAGAAGAGAAGGGGACTGTTTGGGGTGCCTCTCTGCAGCCTCCCCGTGCTGGGTGGAA 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 CACAGAAGAGAAGGGGACTGTTTGGGGTGCCTCTCTGCAGCCTCCCCGTGCTGGGTGGAA 2400

Qy       2401 GCACGGTTACTGTGTTCTCTAATGTTCATGTATTTAAAATGATTTCTTTCTAAAGATGTA 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 GCACGGTTACTGTGTTCTCTAATGTTCATGTATTTAAAATGATTTCTTTCTAAAGATGTA 2460

Qy       2461 ACCTCCACACCTTTCTCCAGATTGGGTGACTCTTTTCTAAAGGTGGTGGGAGTATCTGTC 2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 ACCTCCACACCTTTCTCCAGATTGGGTGACTCTTTTCTAAAGGTGGTGGGAGTATCTGTC 2520

Qy       2521 GGGGTGGTGTGGCCCTTGGATGGGTCAGGTGGGTGTGAGAGGTCCTGGGGAGGTGGGCGT 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 GGGGTGGTGTGGCCCTTGGATGGGTCAGGTGGGTGTGAGAGGTCCTGGGGAGGTGGGCGT 2580

Qy       2581 TGAGCTCAAAGTTGTCCTACTGCCATGTTTTTGTACCTGAAATAAAGCATATTTTGCACT 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 TGAGCTCAAAGTTGTCCTACTGCCATGTTTTTGTACCTGAAATAAAGCATATTTTGCACT 2640

Qy       2641 TGTTACTGTACCATAGTGCGGACGAGAAGTCTGTATGTGGGATCTGTGCTTGGGTTAGAA 2700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 TGTTACTGTACCATAGTGCGGACGAGAAGTCTGTATGTGGGATCTGTGCTTGGGTTAGAA 2700

Qy       2701 TGCAAATAAAACTCACATTTGTAAGAAAAAAAAAAAAAAATAAAAAGATGCGGCC 2754
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 TGCAAATAAAACTCACATTTGTAAGAAAAAAAAAAAAAAATAAAAAGATGCGGCC 2754
```

RESULT 2
ABT07523
ID ABT07523 standard; cDNA; 2754 BP.
XX
AC ABT07523;
XX
DT 14-NOV-2002 (first entry)
XX
DE Human breast cancer associated coding sequence SEQ ID NO: 2.
XX
KW Human; breast specific gene; breast specific protein; breast cancer;
KW gene therapy; cytostatic; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200264611-A1.
XX
PD 22-AUG-2002.
XX
PF 12-FEB-2002; 2002WO-US004197.
XX
PR 13-FEB-2001; 2001US-0268292P.
XX
PA (DIAD-) DIADEXUS INC.
XX
PI Salceda S, Macina RA, Hu P, Recipon H, Karra K, Cafferkey R;
PI Sun Y, Liu C;
XX
DR WPI; 2002-657582/70.
XX
PT New breast specific nucleic acids and proteins, useful for identifying,
PT diagnosing, monitoring, staging, imaging, and treating breast cancer and
PT non-cancerous disease states in breast tissue, and in gene therapy.
XX
PS Claim 1; Page 148-150; 367pp; English.
XX
CC The present invention provides human breast specific coding sequences and
CC proteins. These can be used in the diagnosis and treatment of breast
CC cancer and non-cancerous diseases of the breast. The present sequence is
CC a coding sequence of the invention
XX
SQ Sequence 2754 BP; 557 A; 720 C; 753 G; 724 T; 0 U; 0 Other;

Query Match 100.0%; Score 2754; DB 6; Length 2754;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2754; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GCCAGAAGCAGCCTCAGCTTGGCAAGGTGTGGAGATGACTGCTGTTCCCTTCGCATTTGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCCAGAAGCAGCCTCAGCTTGGCAAGGTGTGGAGATGACTGCTGTTCCCTTCGCATTTGG 60

Qy         61 GGAAAACAGGCTCCCTCGGTAGCTCGATGATCCTCTTTTGATCTTGTGTGACCTCCTGGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAAAACAGGCTCCCTCGGTAGCTCGATGATCCTCTTTTGATCTTGTGTGACCTCCTGGA 120

Qy        121 GAGTGGATGACGCTGGTGGCCTTAGCTTTTCTAGACAGTGTAAATTGCACTGGGCGATGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GAGTGGATGACGCTGGTGGCCTTAGCTTTTCTAGACAGTGTAAATTGCACTGGGCGATGT 180

Qy        181 CCCCAGAGCAGGGCAAGGTCTCTAGAGCGGGTCTCCCACATGACTGGCTTCACACAGGCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCCCAGAGCAGGGCAAGGTCTCTAGAGCGGGTCTCCCACATGACTGGCTTCACACAGGCA 240

Qy        241 CTTCCGCTCGGGTTGCATGCTCTGTGTCATCTTACCGGTCCAGGGTTGCAGGTAGGAAAT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTTCCGCTCGGGTTGCATGCTCTGTGTCATCTTACCGGTCCAGGGTTGCAGGTAGGAAAT 300

Qy        301 GTTTGTACCCTCTTCTGATTGCCACCTCCTTCCCATCGCCCCTTAGGGACAGGGCTTGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTTTGTACCCTCTTCTGATTGCCACCTCCTTCCCATCGCCCCTTAGGGACAGGGCTTGAG 360

Qy        361 GGCCAGTGAGGCGCTGGTCAGGCACCCCAGGCCTCCTTGGGACCTGCCCAGGGGCACCCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGCCAGTGAGGCGCTGGTCAGGCACCCCAGGCCTCCTTGGGACCTGCCCAGGGGCACCCT 420

Qy        421 GAGAGCTCCTGAAACCCCCACTTAGCTTCCAGACCTTTCTGCAAAAGCTCCTCCTGGCTT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GAGAGCTCCTGAAACCCCCACTTAGCTTCCAGACCTTTCTGCAAAAGCTCCTCCTGGCTT 480

Qy        481 TCCTCCCTCCCCCAATCTATGGGTCACAGCTAACAGATCTGAGGGCAACTGCTGTGCTAG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCTCCCTCCCCCAATCTATGGGTCACAGCTAACAGATCTGAGGGCAACTGCTGTGCTAG 540

Qy        541 TGGCCAGGGCTGCACCTGCCATCCCCGGCTCTGCCACTTTAGGGCCTTCTAGAGGCAGTG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TGGCCAGGGCTGCACCTGCCATCCCCGGCTCTGCCACTTTAGGGCCTTCTAGAGGCAGTG 600

Qy        601 TCCTTAGGAAGTAGCTCTGAGGCATGGGTTTTCTGCTCCTGTGCAGGGCAGCTGATGGGA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TCCTTAGGAAGTAGCTCTGAGGCATGGGTTTTCTGCTCCTGTGCAGGGCAGCTGATGGGA 660

Qy        661 TAAGGTGGGGAAGGACGGTCAGTGCTTGGGCCCCAGCTGGCCAGCCTGGCGATGGGGAAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TAAGGTGGGGAAGGACGGTCAGTGCTTGGGCCCCAGCTGGCCAGCCTGGCGATGGGGAAA 720

Qy        721 CCAAACCATGTCCCCCAGCGAAGGGCCAGAGTGGGAACCTGTCCTCATGCCCTTCGTCCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        721 CCAAACCATGTCCCCCAGCGAAGGGCCAGAGTGGGAACCTGTCCTCATGCCCTTCGTCCT 780
Qy        781 GAGGAGCCCTGAGGTGGGCAGCAGGGGCCAGGGGAAGTTTTCAGGCCTTCATCAAAGAGA 840
Db        781 GAGGAGCCCTGAGGTGGGCAGCAGGGGCCAGGGGAAGTTTTCAGGCCTTCATCAAAGAGA 840
Qy        841 ACAACATCCTCAGCTCCGCACCCCTCATCCTGTATCAGCACTTACCGGTGTGTGACTGCC 900
Db        841 ACAACATCCTCAGCTCCGCACCCCTCATCCTGTATCAGCACTTACCGGTGTGTGACTGCC 900
Qy        901 CTTGTCAGCTAGCATACGGTGGGCCCACCTGGCCCACTGGCTGTTTATGCCACTGATTTA 960
Db        901 CTTGTCAGCTAGCATACGGTGGGCCCACCTGGCCCACTGGCTGTTTATGCCACTGATTTA 960
Qy        961 TGATAGGGAATATTATCTTTGAACCCAATGAAGTGTTTTCTCCCCCATCACAAAAAAAAAA 1020
Db        961 TGATAGGGAATATTATCTTTGAACCCAATGAAGTGTTTTCTCCCCCATCACAAAAAAAAAA 1020
Qy       1021 AATTCTTATTTTTAGTAGACATGTATTTACCAAAAATATGTACTCAATTATTGTATTTTG 1080
Db       1021 AATTCTTATTTTTAGTAGACATGTATTTACCAAAAATATGTACTCAATTATTGTATTTTG 1080
Qy       1081 GATTTTATCAATTTAAAAATTGTGGAAATTTGTTTGCTCTTACGCCAACATAATATTGAT 1140
Db       1081 GATTTTATCAATTTAAAAATTGTGGAAATTTGTTTGCTCTTACGCCAACATAATATTGAT 1140
Qy       1141 TTTGCCTCTTGGCTCTGAAAGCCCAAAATATTTACCGTCTAGCCCGTTACAGAAAAAGTC 1200
Db       1141 TTTGCCTCTTGGCTCTGAAAGCCCAAAATATTTACCGTCTAGCCCGTTACAGAAAAAGTC 1200
Qy       1201 TGCTGACTACTGAGCCAGACCTCCATTACCTCCATCCCTGTTGGATTATTTAAAGAAAGC 1260
Db       1201 TGCTGACTACTGAGCCAGACCTCCATTACCTCCATCCCTGTTGGATTATTTAAAGAAAGC 1260
Qy       1261 CTCAGACAGTAAGGGCTTTTTTAAAAGAATAAAATGACTTGGTTTGCGCTTGGAAGCAGG 1320
Db       1261 CTCAGACAGTAAGGGCTTTTTTAAAAGAATAAAATGACTTGGTTTGCGCTTGGAAGCAGG 1320
Qy       1321 GGAAGCATTCAGATGAGCGGTTTCTGCATTAACCCTGCCTATCACGCATCTCGTGTCCTG 1380
Db       1321 GGAAGCATTCAGATGAGCGGTTTCTGCATTAACCCTGCCTATCACGCATCTCGTGTCCTG 1380
Qy       1381 TGTGGCTGGCGAGCCCCCCTTGGAAGGTTCTGGTGCTTCAGCTGGCTCCTGCAGAGTCCA 1440
Db       1381 TGTGGCTGGCGAGCCCCCCTTGGAAGGTTCTGGTGCTTCAGCTGGCTCCTGCAGAGTCCA 1440
Qy       1441 CCCCGCCTCGTGGTGGGAATGCAGAGCCCTTTGCTTTCCTTCTTGCCGCCTGCTTCCTGT 1500
Db       1441 CCCCGCCTCGTGGTGGGAATGCAGAGCCCTTTGCTTTCCTTCTTGCCGCCTGCTTCCTGT 1500
Qy       1501 TCCTGGGGACCCGCTGGGCCTTTGGTCTGCATCCCCTGGCCAGGTCCCTCAGGGTTGATG 1560
Db       1501 TCCTGGGGACCCGCTGGGCCTTTGGTCTGCATCCCCTGGCCAGGTCCCTCAGGGTTGATG 1560
Qy       1561 CGTGGAGAAGGACTTTGAGCAGTGGTGGGCAGCAGTGGCCTCCTGGCCAGCTCACACTCT 1620
Db       1561 CGTGGAGAAGGACTTTGAGCAGTGGTGGGCAGCAGTGGCCTCCTGGCCAGCTCACACTCT 1620
Qy       1621 TGTCCTGGGAGGGGCAGCCTGATCTCACCTCCACCTAGTACCTTGGGGACTGAGGACCTT 1680
Db       1621 TGTCCTGGGAGGGGCAGCCTGATCTCACCTCCACCTAGTACCTTGGGGACTGAGGACCTT 1680
Qy       1681 TTGGCTTCTCTGGAGCCTGCAAGCCTCTTCCCATGTGTCCAGCTGCTCTTCCTGCTACAA 1740
Db       1681 TTGGCTTCTCTGGAGCCTGCAAGCCTCTTCCCATGTGTCCAGCTGCTCTTCCTGCTACAA 1740
Qy       1741 AGGGGACTGCTCACAGTGGCCTCAGCTTGGTGGTTTTGAGGGGCCGCCCCCCGGCCCTCC 1800
Db       1741 AGGGGACTGCTCACAGTGGCCTCAGCTTGGTGGTTTTGAGGGGCCGCCCCCCGGCCCTCC 1800
Qy       1801 ATAAGGGTATCCTGGGCCTGAGAATTCTGCATCTGCCATTGGAGGATGGACAGCCTCAAA 1860
Db       1801 ATAAGGGTATCCTGGGCCTGAGAATTCTGCATCTGCCATTGGAGGATGGACAGCCTCAAA 1860
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Qy       1861 TGGAAGGAGTCCCACGGGAGATGGGTCCGAGGTCCGGCTGTGGCCATCCAGCCCCCTGTG 1920
Db       1861 TGGAAGGAGTCCCACGGGAGATGGGTCCGAGGTCCGGCTGTGGCCATCCAGCCCCCTGTG 1920
Qy       1921 GCTTGTCCAGCCTCTGTGCACCCCTGGTGTCTTCACTCCAGGGGCAGACAGCAGCCACTG 1980
Db       1921 GCTTGTCCAGCCTCTGTGCACCCCTGGTGTCTTCACTCCAGGGGCAGACAGCAGCCACTG 1980
Qy       1981 CAGTTCCTTTCTTCGTGAGTAACAGTAGTGATAGCAGCTGGGGCTAACAGGCTAGGCTTT 2040
Db       1981 CAGTTCCTTTCTTCGTGAGTAACAGTAGTGATAGCAGCTGGGGCTAACAGGCTAGGCTTT 2040
Qy       2041 GTGTTCTGCGCATTTGGTCAGCTTCTCACTCGATCCTCCCTAAAGCAATGGGGAGGCCCC 2100
Db       2041 GTGTTCTGCGCATTTGGTCAGCTTCTCACTCGATCCTCCCTAAAGCAATGGGGAGGCCCC 2100
Qy       2101 CACTAGCCCAGTTTTCAGGAAGTCAACTGGGAGGTTAGATGGGGGCCAGGGTCCCACAGC 2160
Db       2101 CACTAGCCCAGTTTTCAGGAAGTCAACTGGGAGGTTAGATGGGGGCCAGGGTCCCACAGC 2160
Qy       2161 TACTGATGGCCCGAGCCAGGTTGAGCTTCCTGGTGTCCAGTCCGGATCCCACTTGCAGAT 2220
Db       2161 TACTGATGGCCCGAGCCAGGTTGAGCTTCCTGGTGTCCAGTCCGGATCCCACTTGCAGAT 2220
Qy       2221 CTCATGCTCTCAGATAGGTGGGACAAGTTCTTTTGTCACAGTGCTGGCTCTGTCCTGAGG 2280
Db       2221 CTCATGCTCTCAGATAGGTGGGACAAGTTCTTTTGTCACAGTGCTGGCTCTGTCCTGAGG 2280
Qy       2281 CCTCATTGCTGGCTGGGTGTGCTCTGCTGGGAAAAGCTTTGCGGGGGCTTGCTTGGTTAAC 2340
Db       2281 CCTCATTGCTGGCTGGGTGTGCTCTGCTGGGAAAAGCTTTGCGGGGGCTTGCTTGGTTAAC 2340
Qy       2341 CACAGAAGAGAAGGGGACTGTTTGGGGTGCCTCTCTGCAGCCTCCCCGTGCTGGGTGGAA 2400
Db       2341 CACAGAAGAGAAGGGGACTGTTTGGGGTGCCTCTCTGCAGCCTCCCCGTGCTGGGTGGAA 2400
Qy       2401 GCACGGTTACTGTGTTCTCTAATGTTCATGTATTTAAAATGATTTCTTTCTAAAGATGTA 2460
Db       2401 GCACGGTTACTGTGTTCTCTAATGTTCATGTATTTAAAATGATTTCTTTCTAAAGATGTA 2460
Qy       2461 ACCTCCACACCTTTCTCCAGATTGGGTGACTCTTTTCTAAAGGTGGTGGGAGTATCTGTC 2520
Db       2461 ACCTCCACACCTTTCTCCAGATTGGGTGACTCTTTTCTAAAGGTGGTGGGAGTATCTGTC 2520
Qy       2521 GGGGTGGTGTGGCCCTTGGATGGGTCAGGTGGGTGTGAGAGGTCCTGGGGAGGTGGGCGT 2580
Db       2521 GGGGTGGTGTGGCCCTTGGATGGGTCAGGTGGGTGTGAGAGGTCCTGGGGAGGTGGGCGT 2580
Qy       2581 TGAGCTCAAAGTTGTCCTACTGCCATGTTTTTGTACCTGAAATAAAGCATATTTTGCACT 2640
Db       2581 TGAGCTCAAAGTTGTCCTACTGCCATGTTTTTGTACCTGAAATAAAGCATATTTTGCACT 2640
Qy       2641 TGTTACTGTACCATAGTGCGGACGAGAAGTCTGTATGTGGGATCTGTGCTTGGGTTAGAA 2700
Db       2641 TGTTACTGTACCATAGTGCGGACGAGAAGTCTGTATGTGGGATCTGTGCTTGGGTTAGAA 2700
Qy       2701 TGCAAATAAAACTCACATTTGTAAGAAAAAAAAAAAAAAATAAAAAGATGCGGCC 2754
Db       2701 TGCAAATAAAACTCACATTTGTAAGAAAAAAAAAAAAAATAAAAAGATGCGGCC 2754
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RESULT 3
ABX92049/c
ID   ABX92049 standard; cDNA; 2399 BP.
XX
AC   ABX92049;
XX
DT   08-MAY-2003  (first entry)
XX
DE   Lung specific nucleic acid (LSNA) #91.
XX
KW   Human; gene therapy; vaccine; lung specific antigen; cancer diagnosis;
```

KW cancer monitoring; cancer staging; cancer imaging; lung cancer;
KW non-cancerous diseases of the lung; transgenic animal; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200268633-A2.
XX
PD 06-SEP-2002.
XX
PF 21-NOV-2001; 2001WO-US043612.
XX
PR 22-NOV-2000; 2000US-0252500P.
XX
PA (DIAD-) DIADEXUS INC.
XX
PI Macina RA, Recipon H, Chen S, Sun Y, Liu C;
XX
DR WPI; 2002-713376/77.
XX
PT New isolated human nucleic acid molecule and polypeptide, useful for
PT identifying, diagnosing, monitoring, staging, imaging and treating lung
PT cancer and non-cancerous diseases of the lung.
XX
PS Claim 1; Page 238-240; 389pp; English.
XX
CC The invention describes an isolated human nucleic acid (I) encoding any
CC of 120 10-1533 residue amino acid sequences (S1), given in the
CC specification, comprising any of 164 179-12421 base pair sequences (S2),
CC given in the specification. The methods and compositions of the present
CC invention are useful for identifying, diagnosing, monitoring, staging,
CC imaging and treating lung cancer and non-cancerous diseases of the lung.
CC They are also used for identifying lung tissue, monitoring and
CC identifying and/or designing antagonists of the polypeptide of the
CC invention, gene therapy, production of transgenic animals and production
CC of engineered lung tissue for treatment and research. This sequence
CC encodes a lung specific nucleic acid
XX
SQ Sequence 2399 BP; 631 A; 653 C; 622 G; 493 T; 0 U; 0 Other;

Query Match 87.1%; Score 2397.4; DB 6; Length 2399;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2398; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy        356 TTGAGGGCCAGTGAGGCGCTGGTCAGGCACCCCAGGCCTCCTTGGGACCTGCCCAGGGGC 415
              ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db       2399 TTGAGGGCCAGTGAGGTGCTGGTCAGGCACCCCAGGCCTCCTTGGGACCTGCCCAGGGGC 2340

Qy        416 ACCCTGAGAGCTCCTGAAACCCCCACTTAGCTTCCAGACCTTTCTGCAAAAGCTCCTCCT 475
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2339 ACCCTGAGAGCTCCTGAAACCCCCACTTAGCTTCCAGACCTTTCTGCAAAAGCTCCTCCT 2280

Qy        476 GGCTTTCCTCCCTCCCCCAATCTATGGGTCACAGCTAACAGATCTGAGGGCAACTGCTGT 535
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2279 GGCTTTCCTCCCTCCCCCAATCTATGGGTCACAGCTAACAGATCTGAGGGCAACTGCTGT 2220

Qy        536 GCTAGTGGCCAGGGCTGCACCTGCCATCCCCGGCTCTGCCACTTTAGGGCCTTCTAGAGG 595
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2219 GCTAGTGGCCAGGGCTGCACCTGCCATCCCCGGCTCTGCCACTTTAGGGCCTTCTAGAGG 2160

Qy        596 CAGTGTCCTTAGGAAGTAGCTCTGAGGCATGGGTTTTCTGCTCCTGTGCAGGGCAGCTGA 655
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2159 CAGTGTCCTTAGGAAGTAGCTCTGAGGCATGGGTTTTCTGCTCCTGTGCAGGGCAGCTGA 2100

Qy        656 TGGGATAAGGTGGGGAAGGACGGTCAGTGCTTGGGCCCCAGCTGGCCAGCCTGGCGATGG 715
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2099 TGGGATAAGGTGGGGAAGGACGGTCAGTGCTTGGGCCCCAGCTGGCCAGCCTGGCGATGG 2040

Qy        716 GGAAACCAAACCATGTCCCCCAGCGAAGGGCCAGAGTGGGAACCTGTCCTCATGCCCTTC 775
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2039 GGAAACCAAACCATGTCCCCCAGCGAAGGGCCAGAGTGGGAACCTGTCCTCATGCCCTTC 1980

Qy        776 GTCCTGAGGAGCCCTGAGGTGGGCAGCAGGGGCCAGGGGAAGTTTTCAGGCCTTCATCAA 835
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1979 GTCCTGAGGAGCCCTGAGGTGGGCAGCAGGGGCCAGGGGAAGTTTTCAGGCCTTCATCAA 1920

Qy        836 AGAGAACAACATCCTCAGCTCCGCACCCCTCATCCTGTATCAGCACTTACCGGTGTGTGA 895
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1919 AGAGAACAACATCCTCAGCTCCGCACCCCTCATCCTGTATCAGCACTTACCGGTGTGTGA 1860

Qy        896 CTGCCCTTGTCAGCTAGCATACGGTGGGCCCACCTGGCCCACTGGCTGTTTATGCCACTG 955
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1859 CTGCCCTTGTCAGCTAGCATACGGTGGGCCCACCTGGCCCACTGGCTGTTTATGCCACTG 1800

Qy        956 ATTTATGATAGGGAATATTATCTTTGAACCCAATGAAGTGTTTTCTCCCCCATCACAAAA 1015
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1799 ATTTATGATAGGGAATATTATCTTTGAACCCAATGAAGTGTTTTCTCCCCCATCACAAAA 1740

Qy       1016 AAAAAAATTCTTATTTTTAGTAGACATGTATTTACCAAAAATATGTACTCAATTATTGTA 1075
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1739 AAAAAAATTCTTATTTTTAGTAGACATGTATTTACCAAAAATATGTACTCAATTATTGTA 1680

Qy       1076 TTTTGGATTTTATCAATTTAAAAATTGTGGAAATTTGTTTGCTCTTACGCCAACATAATA 1135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1679 TTTTGGATTTTATCAATTTAAAAATTGTGGAAATTTGTTTGCTCTTACGCCAACATAATA 1620

Qy       1136 TTGATTTTGCCTCTTGGCTCTGAAAGCCCAAAATATTTACCGTCTAGCCCGTTACAGAAA 1195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1619 TTGATTTTGCCTCTTGGCTCTGAAAGCCCAAAATATTTACCGTCTAGCCCGTTACAGAAA 1560

Qy       1196 AAGTCTGCTGACTACTGAGCCAGACCTCCATTACCTCCATCCCTGTTGGATTATTTAAAG 1255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1559 AAGTCTGCTGACTACTGAGCCAGACCTCCATTACCTCCATCCCTGTTGGATTATTTAAAG 1500

Qy       1256 AAAGCCTCAGACAGTAAGGGCTTTTTTAAAAGAATAAAATGACTTGGTTTGCGCTTGGAA 1315
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1499 AAAGCCTCAGACAGTAAGGGCTTTTTTAAAAGAATAAAATGACTTGGTTTGCGCTTGGAA 1440

Qy       1316 GCAGGGGAAGCATTCAGATGAGCGGTTTCTGCATTAACCCTGCCTATCACGCATCTCGTG 1375
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1439 GCAGGGGAAGCATTCAGATGAGCGGTTTCTGCATTAACCCTGCCTATCACGCATCTCGTG 1380

Qy       1376 TCCTGTGTGGCTGGCGAGCCCCCCTTGGAAGGTTCTGGTGCTTCAGCTGGCTCCTGCAGA 1435
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1379 TCCTGTGTGGCTGGCGAGCCCCCCTTGGAAGGTTCTGGTGCTTCAGCTGGCTCCTGCAGA 1320

Qy       1436 GTCCACCCCGCCTCGTGGTGGGAATGCAGAGCCCTTTGCTTTCCTTCTTGCCGCCTGCTT 1495
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1319 GTCCACCCCGCCTCGTGGTGGGAATGCAGAGCCCTTTGCTTTCCTTCTTGCCGCCTGCTT 1260

Qy       1496 CCTGTTCCTGGGGACCCGCTGGGCCTTTGGTCTGCATCCCCTGGCCAGGTCCCTCAGGGT 1555
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1259 CCTGTTCCTGGGGACCCGCTGGGCCTTTGGTCTGCATCCCCTGGCCAGGTCCCTCAGGGT 1200

Qy       1556 TGATGCGTGGAGAAGGACTTTGAGCAGTGGTGGGCAGCAGTGGCCTCCTGGCCAGCTCAC 1615
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1199 TGATGCGTGGAGAAGGACTTTGAGCAGTGGTGGGCAGCAGTGGCCTCCTGGCCAGCTCAC 1140

Qy       1616 ACTCTTGTCCTGGGAGGGGCAGCCTGATCTCACCTCCACCTAGTACCTTGGGGACTGAGG 1675
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1139 ACTCTTGTCCTGGGAGGGGCAGCCTGATCTCACCTCCACCTAGTACCTTGGGGACTGAGG 1080

Qy       1676 ACCTTTTGGCTTCTCTGGAGCCTGCAAGCCTCTTCCCATGTGTCCAGCTGCTCTTCCTGC 1735
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1079 ACCTTTTGGCTTCTCTGGAGCCTGCAAGCCTCTTCCCATGTGTCCAGCTGCTCTTCCTGC 1020

Qy       1736 TACAAAGGGGACTGCTCACAGTGGCCTCAGCTTGGTGGTTTTGAGGGGCCGCCCCCCGGC 1795
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1019 TACAAAGGGGACTGCTCACAGTGGCCTCAGCTTGGTGGTTTTGAGGGGCCGCCCCCCGGC 960

Qy       1796 CCTCCATAAGGGTATCCTGGGCCTGAGAATTCTGCATCTGCCATTGGAGGATGGACAGCC 1855
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        959 CCTCCATAAGGGTATCCTGGGCCTGAGAATTCTGCATCTGCCATTGGAGGATGGACAGCC 900

Qy       1856 TCAAATGGAAGGAGTCCCACGGGAGATGGGTCCGAGGTCCGGCTGTGGCCATCCAGCCCC 1915
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        899 TCAAATGGAAGGAGTCCCACGGGAGATGGGTCCGAGGTCCGGCTGTGGCCATCCAGCCCC 840
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Qy       1916 CTGTGGCTTGTCCAGCCTCTGTGCACCCCTGGTGTCTTCACTCCAGGGGCAGACAGCAGC 1975
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        839 CTGTGGCTTGTCCAGCCTCTGTGCACCCCTGGTGTCTTCACTCCAGGGGCAGACAGCAGC 780

Qy       1976 CACTGCAGTTCCTTTCTTCGTGAGTAACAGTAGTGATAGCAGCTGGGGCTAACAGGCTAG 2035
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        779 CACTGCAGTTCCTTTCTTCGTGAGTAACAGTAGTGATAGCAGCTGGGGCTAACAGGCTAG 720

Qy       2036 GCTTTGTGTTCTGCGCATTTGGTCAGCTTCTCACTCGATCCTCCCTAAAGCAATGGGGAG 2095
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        719 GCTTTGTGTTCTGCGCATTTGGTCAGCTTCTCACTCGATCCTCCCTAAAGCAATGGGGAG 660

Qy       2096 GCCCCCACTAGCCCAGTTTTCAGGAAGTCAACTGGGAGGTTAGATGGGGGCCAGGGTCCC 2155
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        659 GCCCCCACTAGCCCAGTTTTCAGGAAGTCAACTGGGAGGTTAGATGGGGGCCAGGGTCCC 600

Qy       2156 ACAGCTACTGATGGCCCGAGCCAGGTTGAGCTTCCTGGTGTCCAGTCCGGATCCCACTTG 2215
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        599 ACAGCTACTGATGGCCCGAGCCAGGTTGAGCTTCCTGGTGTCCAGTCCGGATCCCACTTG 540

Qy       2216 CAGATCTCATGCTCTCAGATAGGTGGGACAAGTTCTTTTGTCACAGTGCTGGCTCTGTCC 2275
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        539 CAGATCTCATGCTCTCAGATAGGTGGGACAAGTTCTTTTGTCACAGTGCTGGCTCTGTCC 480

Qy       2276 TGAGGCCTCATTGCTGGCTGGGTGTGCTCTGCTGGGAAAAGCTTTGCGGGGCTTGCTTGG 2335
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        479 TGAGGCCTCATTGCTGGCTGGGTGTGCTCTGCTGGGAAAAGCTTTGCGGGGCTTGCTTGG 420

Qy       2336 TTAACCACAGAAGAGAAGGGGACTGTTTGGGGTGCCTCTCTGCAGCCTCCCCGTGCTGGG 2395
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        419 TTAACCACAGAAGAGAAGGGGACTGTTTGGGGTGCCTCTCTGCAGCCTCCCCGTGCTGGG 360

Qy       2396 TGGAAGCACGGTTACTGTGTTCTCTAATGTTCATGTATTTAAAATGATTTCTTTCTAAAG 2455
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        359 TGGAAGCACGGTTACTGTGTTCTCTAATGTTCATGTATTTAAAATGATTTCTTTCTAAAG 300

Qy       2456 ATGTAACCTCCACACCTTTCTCCAGATTGGGTGACTCTTTTCTAAAGGTGGTGGGAGTAT 2515
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        299 ATGTAACCTCCACACCTTTCTCCAGATTGGGTGACTCTTTTCTAAAGGTGGTGGGAGTAT 240

Qy       2516 CTGTCGGGGTGGTGTGGCCCTTGGATGGGTCAGGTGGGTGTGAGAGGTCCTGGGGAGGTG 2575
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 CTGTCGGGGTGGTGTGGCCCTTGGATGGGTCAGGTGGGTGTGAGAGGTCCTGGGGAGGTG 180

Qy       2576 GGCGTTGAGCTCAAAGTTGTCCTACTGCCATGTTTTTGTACCTGAAATAAAGCATATTTT 2635
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        179 GGCGTTGAGCTCAAAGTTGTCCTACTGCCATGTTTTTGTACCTGAAATAAAGCATATTTT 120

Qy       2636 GCACTTGTTACTGTACCATAGTGCGGACGAGAAGTCTGTATGTGGGATCTGTGCTTGGGT 2695
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        119 GCACTTGTTACTGTACCATAGTGCGGACGAGAAGTCTGTATGTGGGATCTGTGCTTGGGT 60

Qy       2696 TAGAATGCAAATAAAACTCACATTTGTAAGAAAAAAAAAAAAAAATAAAAAGATGCGGCC 2754
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          59 TAGAATGCAAATAAAACTCACATTTGTAAGAAAAAAAAAAAAAAATAAAAAGATGCGGCC 1
```

RESULT 4
ABX92057
ID ABX92057 standard; cDNA; 960 BP.
XX
AC ABX92057;
XX
DT 08-MAY-2003 (first entry)
XX
DE Lung specific nucleic acid (LSNA) #99.
XX
KW Human; gene therapy; vaccine; lung specific antigen; cancer diagnosis;
KW cancer monitoring; cancer staging; cancer imaging; lung cancer;
KW non-cancerous diseases of the lung; transgenic animal; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200268633-A2.
XX
PD 06-SEP-2002.
XX
PF 21-NOV-2001; 2001WO-US043612.
XX
PR 22-NOV-2000; 2000US-0252500P.
XX
PA (DIAD-) DIADEXUS INC.
XX
PI Macina RA, Recipon H, Chen S, Sun Y, Liu C;
XX
DR WPI; 2002-713376/77.
XX
PT New isolated human nucleic acid molecule and polypeptide, useful for
PT identifying, diagnosing, monitoring, staging, imaging and treating lung
PT cancer and non-cancerous diseases of the lung.
XX
PS Claim 1; Page 246; 389pp; English.
XX
CC The invention describes an isolated human nucleic acid (I) encoding any
CC of 120 10-1533 residue amino acid sequences (S1), given in the
CC specification, comprising any of 164 179-12421 base pair sequences (S2),
CC given in the specification. The methods and compositions of the present
CC invention are useful for identifying, diagnosing, monitoring, staging,
CC imaging and treating lung cancer and non-cancerous diseases of the lung.
CC They are also used for identifying lung tissue, monitoring and
CC identifying and/or designing antagonists of the polypeptide of the
CC invention, gene therapy, production of transgenic animals and production
CC of engineered lung tissue for treatment and research. This sequence
CC encodes a lung specific nucleic acid
XX
SQ Sequence 960 BP; 183 A; 351 C; 232 G; 193 T; 0 U; 1 Other;

```
  Query Match             22.2%;  Score 612.4;  DB 6;  Length 960;
  Best Local Similarity   99.4%;  Pred. No. 1e-156;
  Matches  646;  Conservative    0;  Mismatches    1;  Indels    3;  Gaps    3;

Qy       1658 GTACCTTGGGGACTGAGGACCTTTTGGCTTCTCTGGAGCCTGCAAGCCTCTTCCCATGTG 1717
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         41 GTACCTTGGGGACTGAGGACCTTTTGGCTTCTCTGGAGCCTGCAAGCCTCTTCCCATGTG 100

Qy       1718 TCCAGCTGCTCTTCCTGCTACAAAGGGGACTGCTCACAGTGGCCTCAGCTTGGTGGTTTT 1777
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        101 TCCAGCTGCTCTTCCTGCTACAAAGGGGACTGCTCACAGTGGCCTCAGCTTGGTGGTTTT 160

Qy       1778 GAGGGGCCGCCCCCCGGCCCTCCATAAGGGTATCCTGGGCCTGAGAATTCTGCATCTGCC 1837
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        161 GAGGGGCCGCCCCCCGGCCCTCCATAAGGGTATCCTGGGCCTGAGAATTCTGCATCTGCC 220

Qy       1838 ATTGGAGGATGGACAGCCTCAAATGGAAGGAGTCCCACGGGAGATGGGTCCGAGGTCCGG 1897
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        221 ATTGGAGGATGGACAGCCTCAAATGGAAGGAGTCCCACGGGAGATGGGTCCGAGGTCCGG 280

Qy       1898 CTGTGGCCATCCAGCCCCCTGTGGCTTGTCCAGCCTCTGTGCACCCCTGGTGTCTTCACT 1957
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 CTGTGGCCATCCAGCCCCCTGTGGCTTGTCCAGCCTCTGTGCACCCCTGGTGTCTTCACT 340

Qy       1958 CCAGGGGCAGACAGCAGCCACTGCAGTTCCTTTCTTCGTGAGTAACAGTAGTGATAGCAG 2017
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        341 CCAGGGGCAGACAGCAGCCACTGCAGTTCCTTTCTTCGTGAGTAACAGTAGTGATAGCAG 400

Qy       2018 CTGGGGCTAACAGGCTAGGCTTTGTGTTCTGCGCATTTGGTCAGCTTCTCACTCGATCCT 2077
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        401 CTGGGGCTAACAGGCTAGGCTTTGTGTTCTGCGCATTTGGTCAGCTTCTCACTCGATCCT 460

Qy       2078 CCCTAAAGCAATGGGGAGGCCCCCACTAGCCCAGTTTTCAGGAAGTCAACTGGGAGGTTA 2137
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        461 CCCTAAAGCAATGGGGAGGCCCCCACTAGCCCAGTTTTCAGGAAGTCAACTGGGAGGTTA 520

Qy       2138 GATGGGGGCCAGGGTCCCACA-GCTACTGATGGCCCGAGCCAGGTTGAGCTTCCTGGTGT 2196
             |||||||||||||||||||| ||| ||||||||||||||||||||||||||||||||||||
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Db        521 GATGGGGGCCAGGGTCCCACATGCTGCTGATGGCCCGAGCCAGGTTGAGCTTCCTGGTGT 580

Qy       2197 CCAGTCCGGAT-CCCACTTGCAGATCTCATGCTCTCAGATAGGTGGGACAAGTTCTTTTG 2255
              |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db        581 CCAGTCCGGATCCCCACTTGCAGATCTCATGCTCTCAGATAGGTGGGACAAGTTCTTTTG 640

Qy       2256 TCACAGTGCTGG-CTCTGTCCTGAGGCCTCATTGCTGGCTGGGTGTGCTC 2304
              |||||||||||| ||||||||||||||||||||||||||||||||||||
Db        641 TCACAGTGCTGGCCTCTGTCCTGAGGCCTCATTGCTGGCTGGGTGTGCTC 690


RESULT 5
ABV54530
ID   ABV54530 standard; cDNA; 611 BP.
XX
AC   ABV54530;
XX
DT   17-SEP-2002  (first entry)
XX
DE   Human prostate expression marker cDNA 54521.
XX
KW   Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
KW   pharmacogenomic marker; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200160860-A2.
XX
PD   23-AUG-2001.
XX
PF   20-FEB-2001; 2001WO-US005171.
XX
PR   17-FEB-2000; 2000US-0183319P.
PR   16-MAR-2000; 2000US-0189862P.
PR   25-MAY-2000; 2000US-0207454P.
PR   09-JUN-2000; 2000US-0211314P.
PR   18-JUL-2000; 2000US-0219007P.
PR   13-DEC-2000; 2000US-0255281P.
XX
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI   Schlegel R, Endege WO, Monahan JE;
XX
DR   WPI; 2001-662795/76.
XX
PT   Novel isolated nucleic acid molecule associated with cancerous state of
PT   prostate cells and correlating with presence of prostate cancer, useful
PT   for detecting presence of prostate cancer, stage of prostate cancer.
XX
PS   Claim 1; Page 10539-10540; 11750pp; English.
XX
CC   The invention relates to an isolated nucleic acid molecule (I) comprising
CC   a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC   specification or its complement. (I) is useful for: (a) assessing whether
CC   a patient is afflicted with prostate cancer; (b) monitoring the
CC   progression of prostate cancer in a patient; (c) assessing the efficacy
CC   of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC   the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC   (e) selecting a composition for inhibiting prostate cancer in a patient;
CC   (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC   determining whether prostate cancer has metastasized in a patient; (h)
CC   assessing the aggressiveness or indolence of prostate cancer in a patient
CC   ; (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
XX
SQ   Sequence 611 BP; 111 A; 174 C; 164 G; 159 T; 0 U; 3 Other;

  Query Match             20.1%;  Score 554;  DB 5;  Length 611;
  Best Local Similarity   99.5%;  Pred. No. 7.8e-141;
  Matches  565;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;

Qy       1194 AAAAGTCTGCTGACTACTGAGCCAGACCTCCATTACCTCCATCCCTGTTGGATTATTTAA 1253
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         44 AAAAGTCTGCTGACTACTGAGCCAGACCTCCATTACCTCCATCCCTGTTGGATTATTTAA 103

Qy       1254 AGAAAGCCTCAGACAGTAAGGGC-TTTTTTAAAAGAATAAAATGACTTGGTTTGCGCTTG 1312
              ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        104 AGAAAGCCTCAGACAGTAAGGGCTTTTTTTAAAAGAATAAAATGACTTGGTTTGCGCTTG 163

Qy       1313 GAAGCAGGGGAAGCATTCAGATGAGCGGTTTCTGCATTAACCCTGCCTATCACGCATCTC 1372
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        164 GAAGCAGGGGAAGCATTCAGATGAGCGGTTTCTGCATTAACCCTGCCTATCACGCATCTC 223

Qy       1373 GTGTCCTGTGTGGCTGGCGAGCCCCCCTTGGAAGGTTCTGGTGCTTCAGCTGGCTCCTGC 1432
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        224 GTGTCCTGTGTGGCTGGCGAGCCCCCCTTGGAAGGTTCTGGTGCTTCAGCTGGCTCCTGC 283

Qy       1433 AGAGTCCACCCCGCCTCGTGGTGGGAATGCAGAGCCCTTTGCTTTCCTTCTTGCCGCCTG 1492
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        284 AGAGTCCACCCCGCCTCGTGGTGGGAATGCAGAGCCCTTTGCTTTCCTTCTTGCCGCCTG 343

Qy       1493 CTTCCTGTTCCTGGGGACCCGCTGGGCCTTTGGTCTGCATCCCCTGGCCAGGTCCCTCAG 1552
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        344 CTTCCTGTTCCTGGGGACCCGCTGGGCCTTTGGTCTGCATCCCCTGGCCAGGTCCCTCAG 403

Qy       1553 GGTTGATGCGTGGAGAAGGACTTTGAGCAGTGGTGGGCAGCAGTGGCCTCCTGGCCAGCT 1612
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        404 GGTTGATGCGTGGAGAAGGACTTTGAGCAGTGGTGGGCAGCAGTGGCCTCCTGGCCAGCT 463

Qy       1613 CACACTCTTGTCCTGGGAGGGGCAGCCTGATCTCACCTCCACCTAGTACCTTGGGGACTG 1672
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        464 CACACTCTTGTCCTGNGAGGGGCAGCCTGATCTCACCTCCACCTAGTACCTTGGGGACTG 523

Qy       1673 AGGACCTTTTGGCTTCTCTGGAGCCTGCAAGCCTCTTCCCATGTGTCCAGCTGCTCTTCC 1732
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        524 AGGACCTTTTGGCTTCTCTGGAGCCTGCAAGCCTCTTCCCATGTGTNCAGCTGCTCTTCC 583

Qy       1733 TGCTACAAAGGGGACTGCTCACAGTGGC 1760
              ||||||||||||||||||||||||||||
Db        584 TGCTACAAAGGGGACTGCTCACAGTGGC 611


RESULT 6
ABT07522
ID   ABT07522 standard; cDNA; 591 BP.
XX
AC   ABT07522;
XX
DT   14-NOV-2002  (first entry)
XX
DE   Human breast cancer associated coding sequence SEQ ID NO: 1.
XX
KW   Human; breast specific gene; breast specific protein; breast cancer;
KW   gene therapy; cytostatic; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200264611-A1.
XX
PD   22-AUG-2002.
XX
PF   12-FEB-2002; 2002WO-US004197.
XX
PR   13-FEB-2001; 2001US-0268292P.
XX
PA   (DIAD-) DIADEXUS INC.
XX
PI   Salceda S, Macina RA, Hu P, Recipon H, Karra K, Cafferkey R;
PI   Sun Y, Liu C;
XX
DR   WPI; 2002-657582/70.
XX
PT   New breast specific nucleic acids and proteins, useful for identifying,
PT   diagnosing, monitoring, staging, imaging, and treating breast cancer and
PT   non-cancerous disease states in breast tissue, and in gene therapy.
XX
PS   Claim 1; Page 148; 367pp; English.
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XX
CC   The present invention provides human breast specific coding sequences and
CC   proteins. These can be used in the diagnosis and treatment of breast
CC   cancer and non-cancerous diseases of the breast. The present sequence is
CC   a coding sequence of the invention
XX
SQ   Sequence 591 BP; 106 A; 166 C; 172 G; 147 T; 0 U; 0 Other;

  Query Match             17.6%;  Score 483.8;  DB 6;  Length 591;
  Best Local Similarity   97.5%;  Pred. No. 1.3e-121;
  Matches  555;  Conservative    0;  Mismatches    7;  Indels    7;  Gaps    6;

Qy       1735 CTACAAAGGGGACTGCTCACAGTGGCCTCAGCTTGGTGGTTTTGAGGGGCCGCCCCCCGG 1794
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         12 CTACAAAGGGGACTGCTCACAGTGGCCTCAGCTTGGTGGTTTTGAGGGGCCGCCCCCCGG 71

Qy       1795 CCCTCCATAAGGGTATCCTGGGCCTGAGAATTCTGCATCTGCCATTGGA-GGATGGACAG 1853
             |||||||||||||||||||||||||||||||||||||||||||||||| ||||| ||||
Db         72 CCCTCCATAAGGGTATCCTGGGCCTGAGAATTCTGCATCTGCCATTGGATGGATGTACAG 131

Qy       1854 CCTCAAATGGAAG-GAGTCCCACGGGAGATGGGTCCGAGGTCC-GGCTGTGGCCATCCAG 1911
             ||||||||||||| |||||||||||||||||||||||||||| |||||||||||||||||
Db        132 CCTCAAATGGAAGTGAGTCCCACGGGAGATGGGTCCGAGGTCCAGGCTGTGGCCATCCAG 191

Qy       1912 CCCCCTGTGGCTTGTCCAGCCTCTGTGCACCCCTGGTGTCTTCACTCCAGGGGCAGACAG 1971
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        192 CCCCCTGTGGCTTGTCCAGCCTCTGTGCACCCCTGGTGTCTTCACTCCAGGGGCAGACAG 251

Qy       1972 CAGCCACTGCAGTTCCTTTCTTCGTGAG-TAACAGTAGTGATAGCAGCTGGGGCTAACAG 2030
             |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        252 TAGCCACTGCAGTTCCTTTCTTCGTGAGATAACAGTAGTGATAGCAGCTGGGGCTAACAG 311

Qy       2031 GCTAGGCTTTGTGTTCTGCGCATTTGGTCAGCTTCTCACTCGATCCTCCCTAAAGCAATG 2090
             ||||||||| ||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        312 GCTAGGCTTAGTGTCCTGCGCATTTGGTCAGCTTCTCACTCGATCCTCCCTAAAGCAATG 371

Qy       2091 GGGAGGCCCCCCACTAGCCCAGTTTTCAGGAAGTCAACTGGGAGGTTAGATGGGGGCCAG- 2149
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        372 GGGAGGCCCCCCACTAGCCCAGTTTTCAGGAAGTCAACTGGGAGGTTAGATGGGGGCCAGA 431

Qy       2150 GGTCCCACAGCTACTGATGGCCCGAGCCAGGTTGAGCTT--CCTGGTGTCCAGTCCGGAT 2207
             |||||||||||||||||||||||||||||||||||||||  |  | ||||||||||||||
Db        432 GGTCCCACAGCTACTGATGGCCCGAGCCAGGTTGAGCTTTCCTGGATGTCCAGTCCGGAT 491

Qy       2208 CCCACTTGCAGATCTCATGCTCTCAGATAGGTGGGACAAGTTCTTTTGTCACAGTGCTGG 2267
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        492 CCCACTTGCAGATCTCATGCTCTCAGATAGGTGGGACAAGTTCTTTTGTCACAGTGCTGG 551

Qy       2268 CTCTGTCCTGAGGCCTCATTGCTGGCTGG 2296
             |||||||||||||||||||||||||||||
Db        552 CTCTGTCCTGAGGCCTCATTGCTGGCTGG 580


RESULT 7
AAS59058
ID   AAS59058 standard; cDNA; 395 BP.
XX
AC   AAS59058;
XX
DT   16-JAN-2002  (first entry)
XX
DE   Human cancer related cDNA sequence #176.
XX
KW   Human; ss; lung cancer; adenocarcinoma; breast cancer; colon cancer;
KW   prostate cancer; benign prostatic hypertrophy; BHP; cytostatic.
XX
OS   Homo sapiens.
XX
PN   WO200172781-A2.
XX
PD   04-OCT-2001.
XX
PF   27-MAR-2001; 2001WO-US009952.
XX
PR   28-MAR-2000; 2000US-0192583P.
XX
PA   (CHIR ) CHIRON CORP.
PA   (HYSE-) HYSEQ INC.
XX
PI   Williams LT,  Escobedo J,  Innis MA,  Garcia PD,  Sudduth-Klinger J;
PI   Reinhard C,  He Z,  Randazzo F,  Kennedy GC,  Pot D,  Kassam A;
PI   Lamson G,  Drmanac R,  Crkvenjakov R,  Dickson M,  Drmanac S,  Labat I;
PI   Leshkowitz D,  Kita D,  Garcia V,  Jones LW,  Stache-Crain B;
XX
DR   WPI; 2001-626251/72.
XX
PT   New human polynucleotides useful for the treatment and diagnosis of
PT   cancer.
XX
PS   Claim 1; Page 202; 240pp; English.
XX
CC   The invention relates to an isolated polynucleotide comprising a
CC   nucleotide sequence which hybridises to a sequence selected from one of
CC   316 fully defined sequences given in the specification, antisense
CC   molecules complimentary to the sequences, the polypeptides encoded by the
CC   sequences and antibodies raised against the proteins. The nucleic acids
CC   are useful for detecting differentially expressed genes which correlate
CC   with a cancerous state of a mammalian cell i.e. diagnosing cancer
CC   (especially lung cancer, colon cancer, breast cancer, prostate cancer and
CC   adenocarcinoma). Modifying the gene products of of the nucleic acids
CC   results in inhibition of tumour growth. The nucleic acids are also useful
CC   in gene mapping and tissue profiling. The present sequence is one of the
CC   316 cancer related cDNA sequences
XX
SQ   Sequence 395 BP; 70 A; 111 C; 109 G; 105 T; 0 U; 0 Other;

  Query Match             13.0%;  Score 357.4;  DB 4;  Length 395;
  Best Local Similarity   96.9%;  Pred. No. 4.4e-87;
  Matches  375;  Conservative    0;  Mismatches   11;  Indels    1;  Gaps    1;

Qy       1216 CAGACCTCCATTACCTCCATCCCTGTTGGATTATTTAAAGAAAGCCTCAGACAGTAAGGG 1275
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          9 CAGACCTCCATTACCTCCATCCCTGTTGGATTATTTAAAGAAAGCCTCAGACAGTAAGGG 68

Qy       1276 C-TTTTTTAAAAGAATAAAATGACTTGGTTTGCGCTTGGAAGCAGGGGAAGCATTCAGAT 1334
             | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 CTTTTTTTAAAAGAATAAAATGACTTGGTTTGCGCTTGGAAGCAGGGGAAGCATTCAGAT 128

Qy       1335 GAGCGGTTTCTGCATTAACCCTGCCTATCACGCATCTCGTGTCCTGTGTGGCTGGCGAGC 1394
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 GAGCGGTTTCTGCATTAACCCTGCCTATCACGCATCTCGTGTCCTGTGTGGCTGGCGAGC 188

Qy       1395 CCCCCTTGGAAGGTTCTGGTGCTTCAGCTGGCTCCTGCAGAGTCCACCCCGCCTCGTGGT 1454
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 CCCCCTTGGAAGGTTCTGGTGCTTCAGCTGGCTCCTGCAGAGTCCACCCCGCCTCGTGGT 248

Qy       1455 GGGAATGCAGAGCCCTTTGCTTTCCTTCTTGCCGCCTGCTTCCTGTTCCTGGGGACCCGC 1514
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 GGGAATGCAGAGCCCTTTGCTTTCCTTCTTGCCGCCTGCTTCCTGTTCCTGGGGACCCGC 308

Qy       1515 TGGGCCTTTGGTCTGCATCCCCTGGCCAGGTCCCTCAGGGTTGATGCGTGGAGAAGGACT 1574
             |||||||||||||||||||||||||||||||||||||||| |||||| | ||||||||
Db        309 TGGGCCTTTGGTCTGCATCCCCTGGCCAGGTCCCTCAGGGCTGATGCGCGTAGAAGGACT 368

Qy       1575 TTGAGCAGTGGTGGGCAGCAGTGGCCT 1601
             |||||||||||||        || |||
Db        369 TTGAGCAGTGGTGGCAGCACTTGCCCT 395


RESULT 8
ADD49697
ID   ADD49697 standard; cDNA; 295 BP.
XX
AC   ADD49697;
XX
DT   15-JAN-2004  (first entry)
```

XX
DE Human lung cancer associated cDNA 61594667.
XX
KW Human; ss; lung cancer antigen; cytostatic; lung cancer; gene therapy;
KW vaccine; T-cell; tumour.
XX
OS Homo sapiens.
XX
PN US2003194764-A1.
XX
PD 16-OCT-2003.
XX
PF 04-APR-2002; 2002US-00116712.
XX
PR 05-APR-2001; 2001US-0282289P.
PR 05-OCT-2001; 2001US-0327511P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Bangur CS, Switzer A;
XX
DR WPI; 2003-844452/78.
XX
PT New isolated polypeptides and polynucleotides useful for diagnosing,
PT preventing and treating cancer, particularly lung cancer.
XX
PS Claim 1; SEQ ID NO 429; 250pp; English.
XX
CC The invention relates to an isolated polynucleotide (a) comprising any of
CC the 666 fully defined nucleotide sequences appearing as ADD49269 -
CC ADD49935, ADD49936 and ADD49938, complements of (a); sequences of at
CC least 20 contiguous residues of (a); sequences that hybridise to (a)
CC under highly stringent conditions; sequences having at least 75 or 90%
CC identity to (a); or degenerate variants of (a). Also included are an
CC isolated polypeptide ((b)(comprising: sequences encoded by the new
CC polynucleotide; any of the 4 amino acid sequences fully defined in the
CC specification; or sequences having at least 70 or 90% identity to the
CC sequence in (a) or (b)), an expression vector comprising the above
CC polynucleotide operably linked to an expression control sequence, a host
CC cell transformed or transfected with the above expression vector, an
CC isolated antibody, or its antigen-binding fragment, that specifically
CC binds to the above polypeptide, an oligonucleotide that hybridises to the
CC above-mentioned nucleotide sequences under highly stringent conditions, a
CC fusion protein comprising at least one polypeptide cited above, detecting
CC the presence of a cancer in a patient (comprising: obtaining a biological
CC sample from the patient; contacting the biological sample with a binding
CC agent that binds to the polypeptide, or with the oligonucleotide cited
CC above; detecting in the sample an amount of the polypeptide that binds to
CC the binding agent, or an amount of a polynucleotide that hybridises to
CC the oligonucleotide; and comparing the amount of polypeptide, or
CC polynucleotide that hybridises to the oligonucleotide, to a predetermined
CC cut-off value and then determining the presence of a cancer in the
CC patient), a method for stimulating and/or expanding T-cells specific for
CC a tumour protein (comprising contacting T-cells with the above
CC polypeptide, polynucleotide or antigen-presenting cells that express the
CC polynucleotide, under conditions and for a time sufficient to permit the
CC stimulation and/or expansion of T-cells), an isolated T-cell population
CC comprising T-cells prepared by the method, a composition comprising a
CC first component selected from physiological carriers and
CC immunostimulants, and a second component selected from the above
CC polypeptide, polynucleotide, antibody, fusion protein, T-cell population
CC and antigen-presenting cells that express the above polypeptide,
CC stimulating an immune response in a patient (comprising administering to
CC the patient the above composition) treating lung cancer in a patient
CC (comprising administering to the patient the above composition and a
CC diagnostic kit (comprising: at least one oligonucleotide cited above; or
CC at least one antibody cited above and a detection reagent, where the
CC detection reagent comprises a reporter group). The composition and
CC methods are useful in diagnosing, preventing and treating cancer,
CC particularly lung cancer. The present sequence is a lung cancer-
CC associated antigen cDNA of the invention.
XX
SQ Sequence 295 BP; 52 A; 88 C; 88 G; 67 T; 0 U; 0 Other;

Query Match 10.7%; Score 295; DB 10; Length 295;
Best Local Similarity 100.0%; Pred. No. 4.7e-70;
Matches 295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1723 CTGCTCTTCCTGCTACAAAGGGGACTGCTCACAGTGGCCTCAGCTTGGTGGTTTTGAGGG 1782
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CTGCTCTTCCTGCTACAAAGGGGACTGCTCACAGTGGCCTCAGCTTGGTGGTTTTGAGGG 60

Qy       1783 GCCGCCCCCCCGGCCCTCCATAAGGGTATCCTGGGCCTGAGAATTCTGCATCTGCCATTGG 1842
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCGCCCCCCCGGCCCTCCATAAGGGTATCCTGGGCCTGAGAATTCTGCATCTGCCATTGG 120

Qy       1843 AGGATGGACAGCCTCAAATGGAAGGAGTCCCACGGGAGATGGGTCCGAGGTCCGGCTGTG 1902
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AGGATGGACAGCCTCAAATGGAAGGAGTCCCACGGGAGATGGGTCCGAGGTCCGGCTGTG 180

Qy       1903 GCCATCCAGCCCCCTGTGGCTTGTCCAGCCTCTGTGCACCCCTGGTGTCTTCACTCCAGG 1962
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCATCCAGCCCCCTGTGGCTTGTCCAGCCTCTGTGCACCCCTGGTGTCTTCACTCCAGG 240

Qy       1963 GGCAGACAGCAGCCACTGCAGTTCCTTTCTTCGTGAGTAACAGTAGTGATAGCAG 2017
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GGCAGACAGCAGCCACTGCAGTTCCTTTCTTCGTGAGTAACAGTAGTGATAGCAG 295
```

RESULT 9
ABX92048/c
ID ABX92048 standard; cDNA; 251 BP.
XX
AC ABX92048;
XX
DT 08-MAY-2003 (first entry)
XX
DE Lung specific nucleic acid (LSNA) #90.
XX
KW Human; gene therapy; vaccine; lung specific antigen; cancer diagnosis;
KW cancer monitoring; cancer staging; cancer imaging; lung cancer;
KW non-cancerous diseases of the lung; transgenic animal; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200268633-A2.
XX
PD 06-SEP-2002.
XX
PF 21-NOV-2001; 2001WO-US043612.
XX
PR 22-NOV-2000; 2000US-0252500P.
XX
PA (DIAD-) DIADEXUS INC.
XX
PI Macina RA, Recipon H, Chen S, Sun Y, Liu C;
XX
DR WPI; 2002-713376/77.
XX
PT New isolated human nucleic acid molecule and polypeptide, useful for
PT identifying, diagnosing, monitoring, staging, imaging and treating lung
PT cancer and non-cancerous diseases of the lung.
XX
PS Claim 1; Page 238; 389pp; English.
XX
CC The invention describes an isolated human nucleic acid (I) encoding any
CC of 120 10-1533 residue amino acid sequences (S1), given in the
CC specification, comprising any of 164 179-12421 base pair sequences (S2),
CC given in the specification. The methods and compositions of the present
CC invention are useful for identifying, diagnosing, monitoring, staging,
CC imaging and treating lung cancer and non-cancerous diseases of the lung.
CC They are also used for identifying lung tissue, monitoring and
CC identifying and/or designing antagonists of the polypeptide of the
CC invention, gene therapy, production of transgenic animals and production
CC of engineered lung tissue for treatment and research. This sequence
CC encodes a lung specific nucleic acid

```
XX
SQ   Sequence 251 BP; 79 A; 75 C; 54 G; 43 T; 0 U; 0 Other;

  Query Match             8.1%;  Score 224.4;  DB 6;  Length 251;
  Best Local Similarity   98.8%;  Pred. No. 9.4e-51;
  Matches  237;  Conservative    0;  Mismatches    1;  Indels    2;  Gaps    1;

Qy       2381 CCTCCCCGTGCTGGGTGGAAGCACGGTTACTGTGTTCTCTAATGTTCATGTATTTAAAAT 2440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 CCTCCCCGTGCTGGGTGGAAGCACGGTTACTGTGTTCTCTAATGTTCATGTATTTAAAAT 192

Qy       2441 GATTTCTTTCTAAAGATGTAACCTCCACACCTTTCTCCAGATTGGGTGACTCTTTTCTAA 2500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         191 GATTTCTTTCTAAAGATGTAACCTCCACACCTTTCTCCAGATTGGGTGACTCTTTTCTAA 132

Qy       2501 AGGTGGTGGGAGTATCTGTCGGGGTGGTGTGGCCCTTGGATGGGTCAGGTGGGTGTGAGA 2560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         131 AGGTGGTGGGAGTATCTGTCGGGGTGGTGTGGCCCTTGGATGGGTCAGGTGGGTGTGAGA 72

Qy       2561 GGTCCTGGGGAGGT--GGGCGTTGAGCTCAAAGTTGTCCTACTGCCATGTTTTTGTACCT 2618
             ||||||||||||||  |||||||||||||||||||||||||||||||||||||||||||||
Db          71 GGTCCTGGGGAGGTGCGCGCGTTGAGCTCAAAGTTGTCCTACTGCCATGTTTTTGTACCT 12


RESULT 10
AAZ35057
ID   AAZ35057 standard; DNA; 736 BP.
XX
AC   AAZ35057;
XX
DT   28-FEB-2000  (first entry)
XX
DE   Pluripotent cell marker gene L17 DD-PCR product.
XX
KW   Cell differentiation; cell proliferation; cell maintenance; human;
KW   ectoderm-like cell; embryonic stem cell; pluripotent cell; gene therapy;
KW   cell therapy; tissue transplant; organ transplant; xerotransplant;
KW   allotransplant; concomitant transplantation; transgenic animal; L17; ds.
XX
OS   Homo sapiens.
XX
PN   WO9953021-A1.
XX
PD   21-OCT-1999.
XX
PF   09-APR-1999;   99WO-AU000265.
XX
PR   09-APR-1998;   98AU-00002912.
PR   23-SEP-1998;   98AU-00006097.
XX
PA   (BRES-) BRESAGEN LTD.
XX
PI   Bettess MD,  Rathjen PD,  Rathjen J;
XX
DR   WPI; 2000-061970/05.
XX
PT   New isolated biologically active factor capable of influencing
PT   differentiation, proliferation or maintenance of pluripotent cells.
XX
PS   Example 1; Fig 3A; 189pp; English.
XX
CC   This is the nucleotide sequence of a novel partial cDNA, termed L17, that
CC   is differentially expressed between embryonic stem (ES) and primitive
CC   ectoderm-like (EPL) cells. Novel L17, K7 (see AAZ35058) and Psc1 (see
CC   AAZ35059) clones were identified by differential display PCR using RNA
CC   isolated form ES and EPL cells that had been cultured in MEDII+LIF for 2,
CC   4, 6 and 8 days. L17 was highly expressed in ES cells but down regulated
CC   rapidly with EPL formation and maintenance in culture. The expression of
CC   novel pluripotent cell marker genes supports the relationship between EPL
CC   cells and early primitive ectoderm. The invention relates to a novel
CC   biologically active factor capable of influencing the differentiation,
CC   proliferation or maintenance of pluripotent cells. Methods are provided
CC   for producing partially or terminally differentiated cells from
CC   pluripotent cells. The pluripotent cells and partially or terminally
CC   differentiated cells can be used in allo-, concomitant- or xeno-
CC   transplantation, cell therapy, tissue and organ augmentation or
CC   replacement, and gene therapy. They can also be used for producing
CC   chimeric or transgenic animals
XX
SQ   Sequence 736 BP; 202 A; 147 C; 174 G; 213 T; 0 U; 0 Other;

  Query Match             2.8%;  Score 76.6;  DB 3;  Length 736;
  Best Local Similarity   68.5%;  Pred. No. 5.4e-10;
  Matches  191;  Conservative    0;  Mismatches   59;  Indels   29;  Gaps    5;

Qy       2471 CTTTCTCCAGATTGGGTGACTCTTTTCTAAAGGTGGTGGGAGTATCTGTCGGGGTGGTGT 2530
             ||| ||| || | |||||| ||||||||||||||||| ||  | | |    ||  |
Db        483 CTTCCTCTAGGTGGGGTGATTCTTTTCTAAAGGTGGTAGGGTTTTTTAGGTGGTAG---- 538

Qy       2531 GGCCCTTGGATGGGTCAGGTGGGTGTGAGAGGTC-CTGGGGAGGTGGGCGTTGAGCTCAA 2589
                ||  |||||  |  ||||  |||| | ||  ||  | | | ||   | |
Db        539 ----TCCAGACTGGTCAAATATGTGTGGCAGGTCACGGGAAAGGGAGTCATGGAAACCCA 594

Qy       2590 AGTTGTCCTACTGCCA---TGTTTTTGTACCTGAAATAAAGCATATTTTGCACTTGTTAC 2646
                |||||| || |||||   |||||||||||||||||||||||||||||||||||||| |
Db        595 CGTTGTCATAATGCCATGTTGTTTTTGTACCTGAAATAAAGCATATTTTGCACTTGTAAA 654

Qy       2647 TGTACCATAGTGCGGACGAGAAGTCTGTATGTGGGATCTGTGCTTGGGTTAGAATGCAAA 2706
                || |              || |||||||||||| |||||| ||||| ||||||||||
Db        655 TGAA----------------AAATCTGTATGTGGGCTCTGTGC-TGGGTCAGAATGCAAA 697

Qy       2707 TAAAACTCACATTTGTAAGAAAAAAAAAAAAAAATAAAAA 2745
                ||||||      |  || |||||||||||||| |||||
Db        698 TAAAACCATTTGTACTAAAAAAAAAAAAAAAAAAAAAAA 736


RESULT 11
AAK90877/c
ID   AAK90877 standard; DNA; 32038 BP.
XX
AC   AAK90877;
XX
DT   05-NOV-2001  (first entry)
XX
DE   Human digestive system antigen genomic sequence SEQ ID NO: 4453.
XX
KW   Human; digestive system antigen; gene therapy; cancer; appendicitis;
KW   ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;
KW   digestive system disorder; Meckel's diverticulum; ds.
XX
OS   Homo sapiens.
XX
PN   WO200155314-A2.
XX
PD   02-AUG-2001.
XX
PF   17-JAN-2001; 2001WO-US001324.
XX
PR   31-JAN-2000; 2000US-0179065P.
PR   04-FEB-2000; 2000US-0180628P.
PR   24-FEB-2000; 2000US-0184664P.
PR   02-MAR-2000; 2000US-0186350P.
PR   16-MAR-2000; 2000US-0189874P.
PR   17-MAR-2000; 2000US-0190076P.
PR   18-APR-2000; 2000US-0198123P.
PR   19-MAY-2000; 2000US-0205515P.
PR   07-JUN-2000; 2000US-0209467P.
PR   28-JUN-2000; 2000US-0214886P.
PR   30-JUN-2000; 2000US-0215135P.
PR   07-JUL-2000; 2000US-0216647P.
PR   07-JUL-2000; 2000US-0216880P.
PR   11-JUL-2000; 2000US-0217487P.
PR   11-JUL-2000; 2000US-0217496P.
PR   14-JUL-2000; 2000US-0218290P.
PR   26-JUL-2000; 2000US-0220963P.
PR   26-JUL-2000; 2000US-0220964P.
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PR 14-AUG-2000; 2000US-0224518P.
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PR 23-AUG-2000; 2000US-0227009P.
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PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
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PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
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PR 21-SEP-2000; 2000US-0234223P.
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PR 26-SEP-2000; 2000US-0235484P.
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PR 29-SEP-2000; 2000US-0236327P.
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PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
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PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
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PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
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PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-502630/55.
XX
PT Polynucleotides encoding digestive system antigens, useful for
PT diagnosing, treating, preventing and/or prognozing disorders of the
PT digestive system, particularly cancer and cancer metastases.
XX
PS Disclosure; SEQ ID NO 4453; 986pp; English.
XX
CC The present invention provides the protein and coding sequences of a
CC number of human digestive system antigens. These can be used in the
CC diagnosis, treatment and prevention of digestive system disorders,
CC including cancer, Meckel's diverticulum, bacterial or parasitic
CC infections, appendicitis, Hirschsprung's disease, chronic colitis or
CC ulcerative colitis. The present sequence is a genomic DNA fragment
CC encoding a digestive system antigen of the invention
XX
SQ Sequence 32038 BP; 9776 A; 5476 C; 5963 G; 10823 T; 0 U; 0 Other;

Query Match 2.7%; Score 75; DB 4; Length 32038;
Best Local Similarity 65.9%; Pred. No. 1.3e-08;
Matches 147; Conservative 0; Mismatches 60; Indels 16; Gaps 2;

Qy 1013 AAAAAAAAAATTCTTATTTTAGTAGACATGTATTTACCAAAAATATGTACTCAATTATT 1072

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               ||| |   ||||||| |  ||||| ||  ||||     |||||  ||| || ||||||
Db       28877 AAATATTTAATTCTTTCATTAGTAAACCCGTATTACAAAAAAAATTGTTCTAAATTATT 28818

Qy        1073 GTATTTTGGATTTTATCAATTTAAAAATTGTGGAAATTTGTTTGCTCTTACGC------- 1125
               |  ||||| ||||| |||||  ||    | ||| ||||||  || ||||    |
Db       28817 G--TTTTGAATTTTGTCAATAAAATTTTCGTGCAAATTTTATTTCTCTCTAGTTATTTAA 28760

Qy        1126 -------CAACATAATATTGATTTTGCCTCTTGGCTCTGAAAGCCCAAAATATTTACCGT 1178
                      ||  | ||| |    |||| |||||| || |  |||||| ||||||||||   |
Db       28759 GTATCTACATAACAATCTCAGTTTTACCTCTTAGCCCACAAAGCCTAAAATATTTACTAT 28700

Qy        1179 CTAGCCCGTTACAGAAAAAGTCTGCTGACTACTGAGCCAGACC 1221
               || |||| ||| ||||||||| | |||||   |||  | ||| |
Db       28699 CTGGCCCTTTATAGAAAAAGTTTCCTGACCTCTGCCCTAGAGC 28657


RESULT 12
AAK89980/c
ID   AAK89980 standard; DNA; 32038 BP.
XX
AC   AAK89980;
XX
DT   05-NOV-2001  (first entry)
XX
DE   Human digestive system antigen genomic sequence SEQ ID NO: 3556.
XX
KW   Human; digestive system antigen; gene therapy; cancer; appendicitis;
KW   ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;
KW   digestive system disorder; Meckel's diverticulum; ds.
XX
OS   Homo sapiens.
XX
PN   WO200155314-A2.
XX
PD   02-AUG-2001.
XX
PF   17-JAN-2001; 2001WO-US001324.
XX
PR   31-JAN-2000; 2000US-0179065P.
PR   04-FEB-2000; 2000US-0180628P.
PR   24-FEB-2000; 2000US-0184664P.
PR   02-MAR-2000; 2000US-0186350P.
PR   16-MAR-2000; 2000US-0189874P.
PR   17-MAR-2000; 2000US-0190076P.
PR   18-APR-2000; 2000US-0198123P.
PR   19-MAY-2000; 2000US-0205515P.
PR   07-JUN-2000; 2000US-0209467P.
PR   28-JUN-2000; 2000US-0214886P.
PR   30-JUN-2000; 2000US-0215135P.
PR   07-JUL-2000; 2000US-0216647P.
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PR   22-AUG-2000; 2000US-0227182P.
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PR   01-SEP-2000; 2000US-0229287P.
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PR   05-SEP-2000; 2000US-0229509P.
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PR   06-SEP-2000; 2000US-0230437P.
PR   06-SEP-2000; 2000US-0230438P.
PR   08-SEP-2000; 2000US-0231242P.
PR   08-SEP-2000; 2000US-0231243P.
PR   08-SEP-2000; 2000US-0231244P.
PR   08-SEP-2000; 2000US-0231413P.
PR   08-SEP-2000; 2000US-0231414P.
PR   08-SEP-2000; 2000US-0232080P.
PR   08-SEP-2000; 2000US-0232081P.
PR   12-SEP-2000; 2000US-0231968P.
PR   14-SEP-2000; 2000US-0232397P.
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PR   14-SEP-2000; 2000US-0232400P.
PR   14-SEP-2000; 2000US-0232401P.
PR   14-SEP-2000; 2000US-0233063P.
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PR   14-SEP-2000; 2000US-0233065P.
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XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Barash SC,  Ruben SM;
XX
DR   WPI; 2001-502630/55.
XX
PT   Polynucleotides encoding digestive system antigens, useful for
PT   diagnosing, treating, preventing and/or prognozing disorders of the
PT   digestive system, particularly cancer and cancer metastases.
XX
PS   Disclosure; SEQ ID NO 3556; 986pp; English.
XX
CC   The present invention provides the protein and coding sequences of a
CC   number of human digestive system antigens. These can be used in the
CC   diagnosis, treatment and prevention of digestive system disorders,
CC   including cancer, Meckel's diverticulum, bacterial or parasitic
CC   infections, appendicitis, Hirschsprung's disease, chronic colitis or
CC   ulcerative colitis. The present sequence is a genomic DNA fragment
CC   encoding a digestive system antigen of the invention
XX
SQ   Sequence 32038 BP; 9776 A; 5476 C; 5963 G; 10823 T; 0 U; 0 Other;

  Query Match             2.7%;  Score 75;  DB 4;  Length 32038;
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Qy       1073 GTATTTTGGATTTTATCAATTTAAAAATTGTGGAAATTTGTTTGCTCTTACGC------- 1125
              |  ||||| ||||| |||||  ||    | ||| ||||||  || ||||    |
Db      28817 G--TTTTGAATTTTGTCAATAAAATTTTCGTGCAAATTTTATTTCTCTCTAGTTATTTAA 28760

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Db      28759 GTATCTACATAACAATCTCAGTTTTACCTCTTAGCCCACAAAGCCTAAAATATTTACTAT 28700

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Db      28699 CTGGCCCTTTATAGAAAAAGTTTCCTGACCTCTGCCCTAGAGC 28657

RESULT 13
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ID   AAS30028 standard; DNA; 32038 BP.
XX
AC   AAS30028;
XX
DT   21-NOV-2001  (first entry)
XX
DE   Human lung antigen genomic DNA #98.
XX
KW   Lung antigen protein; human; mouse; rabbit; goat; horse; cat; dog;
KW   chicken; sheep; immunosuppressive; antiarthritic; vasotropic;
KW   antirheumatic; antiproliferative; cytostatic; cardiant; neuroprotective;
KW   cerebroprotective; nootropic; antibacterial; virucide; fungicide; cancer;
KW   ophthalmological; vulnerary; gene therapy; autoimmune disease; neoplasm;
KW   hyperproliferative disorder; breast; liver; cardiovascular disorder; ds;
KW   cerebrovascular disorder; nervous system disorder; bacterial infection;
KW   fungal infection; viral infection; ocular disorder; endocrine disorder;
KW   gastrointestinal disorder; renal disorder; respiratory disorder;
KW   wound healing; skin aging; organ transplantation; food preservative;
KW   tissue regeneration; anti-infertility; food additive.
XX
OS   Homo sapiens.
XX
PN   WO200155303-A2.
XX
PD   02-AUG-2001.
XX
PF   17-JAN-2001; 2001WO-US001301.
XX
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PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-457723/49.
XX
PT Isolated polypeptide for treating, preventing and/ or prognosing
PT respiratory disorders related to the lung including lung cancers and also
PT for testing and detection e.g. diagnosis.
XX
PS Claim 1; SEQ ID NO 292; 507pp; English.
XX
CC Sequences AAS29931-AAS30164 represent genomic DNA molecules, which encode
CC the lung antigen polypeptides of the invention. Lung antigen polypeptides
CC and their associated polynucleotides are useful in the diagnosis,
CC treatment and prevention of various types of disorders in e.g. humans,
CC mice, rabbits, goats, horses, cats, dogs, chickens or sheep. A
CC pathological condition can be determined by detecting the presence or
CC absence of a mutation in a lung antigen polynucleotide. The treatable
CC disorders include autoimmune diseases such as rheumatoid arthritis,
CC hyperproliferative disorders such as neoplasms of the breast or liver,
CC cardiovascular disorders such as cardiac arrest, cerebrovascular
CC disorders such as cerebral ischaemia, nervous system disorders such as
CC Alzheimer's disease, infections caused by bacteria, viruses and fungi,
CC ocular disorders such as corneal infection, endocrine disorders such as
CC premature labour and infertility, gastrointestinal disorders such as
CC Crohn's disease, renal disorders such as glomerulonephritis and
CC respiratory disorders such as asthma and pleurisy. The polypeptides can
CC also be used to aid wound healing, to prevent skin aging due to sunburn,
CC to maintain organs before transplantation, to regenerate tissues and in
CC chemotaxis. The polypeptides can also be used as a food additive or
CC preservative to increase or decrease storage capabilities. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences

Query Match 2.7%; Score 75; DB 5; Length 32038;
Best Local Similarity 65.9%; Pred. No. 1.3e-08;
Matches 147; Conservative 0; Mismatches 60; Indels 16; Gaps 2;

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Db     28877 AAATATTTAATTCTTTTCATTAGTAAACCCGTATTACAAAAAAAATTGTTCTAAATTATT 28818

Qy      1073 GTATTTTGGATTTTATCAATTTAAAAATTGTGGAAATTTGTTTGCTCTTACGC------- 1125
             |  ||||| ||||| |||||  ||   | ||| ||||||  || ||||   |
Db     28817 G--TTTTGAATTTTGTCAATAAAATTTTCGTGCAAATTTTATTTCTCTCTAGTTATTTAA 28760

Qy      1126 -------CAACATAATATTGATTTTGCCTCTTGGCTCTGAAAGCCCAAAATATTTACCGT 1178
                    ||  | ||| |   |||| |||||| || |  |||||| ||||||||||  |
Db     28759 GTATCTACATAACAATCTCAGTTTTACCTCTTAGCCCACAAAGCCTAAAATATTTACTAT 28700

Qy      1179 CTAGCCCGTTACAGAAAAAGTCTGCTGACTACTGAGCCAGACC 1221
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Db      28699 CTGGCCCTTTATAGAAAAAGTTTCCTGACCTCTGCCCTAGAGC 28657

RESULT 14
ADB33365/c
ID   ADB33365 standard; DNA; 32038 BP.
XX
AC   ADB33365;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Human novel lung related polypeptide DNA SEQ ID NO 292.
XX
KW   gene therapy; lung antigen; neoplasia; acute myelogenous leukaemia;
KW   adenocarcinoma; respiratory disorder; chronic rhinitis; sinusitis;
KW   immunodeficiency; X-linked agammaglobulinaemia;
KW   X-linked infantile agammaglobulinaemia; inflammatory disorder;
KW   adrenalitis; alveolitis; immune complex disease; serum sickness;
KW   polyarteritis nodosa; bleeding disorder; thrombocytopenia;
KW   Von Willebrand's disease; acquired platelet dysfunction; kidney failure;
KW   multiple myeloma; macrophage related disorder; Gaucher's disease;
KW   Neimann-Pick disease; tumour; colon cancer; pancreatic cancer;
KW   renal disorder; nephritis; bone disorder; Albers-Schonberg disease;
KW   bowleg; muscle disorder; Becker's muscular dystrophy;
KW   Duchenne's muscular dystrophy; nervous disorder; ischaemic lesion;
KW   traumatic lesion; endocrine disorder; Cushing's syndrome;
KW   corticosteroid deficiency; gastrointestinal disorder; dysphagia;
KW   gastric reflux; human; ds.
XX
OS   Homo sapiens.
XX
PN   US2003054368-A1.
XX
PD   20-MAR-2003.
XX
PF   22-FEB-2002; 2002US-00079854.
XX
PR   31-JAN-2000; 2000US-0179065P.
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PR   28-JUN-2000; 2000US-0214886P.
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PR   07-JUL-2000; 2000US-0216647P.
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PR   11-JUL-2000; 2000US-0217487P.
PR   11-JUL-2000; 2000US-0217496P.
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PR   08-NOV-2000; 2000US-0246526P.
PR   08-NOV-2000; 2000US-0246527P.
PR   08-NOV-2000; 2000US-0246528P.
PR   08-NOV-2000; 2000US-0246532P.
PR   08-NOV-2000; 2000US-0246609P.
PR   08-NOV-2000; 2000US-0246610P.
PR   08-NOV-2000; 2000US-0246611P.
PR   08-NOV-2000; 2000US-0246613P.
PR   17-NOV-2000; 2000US-0249207P.
PR   17-NOV-2000; 2000US-0249208P.
PR   17-NOV-2000; 2000US-0249209P.
PR   17-NOV-2000; 2000US-0249210P.
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PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
PR 17-JAN-2001; 2001US-00764878.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM, Barash SC;
XX
DR WPI; 2003-695900/66.
XX
PT Novel isolated lung antigen polypeptides useful for treating, preventing,
PT diagnosing acute myelogenous leukemias, adenocarcinoma, thrombocytopenia,
PT Von Willebrand's disease.
XX
PS Disclosure; SEQ ID NO 292; 178pp; English.
XX
CC The invention relates to an isolated lung antigen polypeptide sequence or
CC encoded sequence in a cDNA clone. The polypeptide and its polynucleotide
CC are useful for treating, preventing, diagnosing and/or prognosing
CC diseases and/or disorders such as pathological cell proliferative
CC neoplasias e.g. acute myelogenous leukaemias, adenocarcinoma; respiratory
CC disorders such as chronic rhinitis, sinusitis; immunodeficiencies such as
CC X-linked agammaglobulinaemia, X-linked infantile agammaglobulinaemia;
CC inflammatory disorders such as adrenalitis, alveolitis; immune complex
CC diseases such as serum sickness, polyarteritis nodosa; bleeding disorders
CC such as thrombocytopenia, Von Willebrand's disease; acquired platelet
CC dysfunction such as kidney failure, multiple myeloma; disorders
CC associated with macrophage numbers and/or macrophage function such as
CC Gaucher's disease, Neimann-Pick disease; tumours such as colon cancer,
CC pancreatic cancer; renal disorders such as kidney failure, nephritis;
CC bone disorders such as Albers-Schonberg disease, bowlegs; muscle
CC disorders such as Becker's muscular dystrophy, Duchenne's muscular
CC dystrophy; nervous disorders such as ischaemic lesions, traumatic lesions
CC ; endocrine disorders such as Cushing's syndrome, corticosteroid

Query Match 2.7%; Score 75; DB 10; Length 32038;
Best Local Similarity 65.9%; Pred. No. 1.3e-08;
Matches 147; Conservative 0; Mismatches 60; Indels 16; Gaps 2;

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Db      28877 AAATATTTAATTCTTTTCATTAGTAAACCCGTATTACAAAAAAAATTGTTCTAAATTATT 28818

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Qy       1126 -------CAACATAATATTGATTTTGCCTCTTGGCTCTGAAAGCCCAAAATATTTACCGT 1178
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              || |||| ||| |||||||||  | |||||  |||  | ||| |
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RESULT 15
ADJ12644
ID ADJ12644 standard; DNA; 32844 BP.
XX
AC ADJ12644;
XX
DT 20-MAY-2004 (first entry)
XX
DE DNA fragment of a BAC clone that encodes a human secreted protein Seq498.
XX
KW human; secreted; cancer; haematopoietic disease; anaemia;
KW multiple myeloma; reproductive system disorder; prostatitis;
KW inguinal hernia; musculoskeletal disease; systemic lupus erythematosus;
KW gout; cardiovascular disease; arrhythmia; hypernatraemia; fetal disease;
KW fetal alcohol syndrome; Down's syndrome; excretory disease;
KW urinary incontinence; renal disorder; neural; sensory disease;
KW Alzheimer's disease; meningitis; respiratory disease; emphysema;
KW occupational lung disease; endocrine disease; diabetes;
KW glomerulonephritis; digestive disease; portal hypertension;
KW irritable bowel syndrome; epithelial disease; scleroderma;
KW epidermolysis bullosa; cytostatic; antianemic; antiarthritic;
KW antiasthmatic; anti-HIV; immunosuppressive; antiinflammatory;
KW antipsoriatic; antibacterial; osteopathic; dermatological; antigout;
KW immunomodulator; antiarrhythmic; cardiant; nootropic; antilipemic;
KW nephrotropic; uropathic; neuroprotective; antiparkinsonian; tranquilizer;
KW antidiabetic; anabolic; hypertensive; vulnerary; ds.
XX
OS Homo sapiens.
XX
PN US2004010132-A1.
XX
PD 15-JAN-2004.
XX
PF 30-OCT-2001; 2001US-00984429.
XX
PR 09-OCT-1997; 97US-0061463P.
PR 09-OCT-1997; 97US-0061527P.
PR 09-OCT-1997; 97US-0061529P.
PR 09-OCT-1997; 97US-0061532P.
PR 09-OCT-1997; 97US-0061536P.
PR 09-OCT-1997; 97US-0071498P.
PR 08-OCT-1998; 98WO-US021142.
PR 08-APR-1999; 99US-00288143.
PR 01-NOV-2000; 2000US-0244591P.
XX
PA (ROSE/) ROSEN C A.
PA (BREW/) BREWER L A.
PA (DUAN/) DUAN R D.
PA (RUBE/) RUBEN S M.
PA (FLOR/) FLORENCE K A.
PA (GREE/) GREENE J M.
PA (YOUN/) YOUNG P E.
PA (FERR/) FERRIE A M.
PA (YUGG/) YU G.
PA (FLOR/) FLORENCE C.
PA (EBNE/) EBNER R.
PA (OLSE/) OLSEN H.
XX
PI Rosen CA, Brewer LA, Duan RD, Ruben SM, Florence KA, Greene JM;
PI Young PE, Ferrie AM, Yu G, Florence C, Ebner R, Olsen H;
XX
DR WPI; 2004-090518/09.
XX
PT New isolated nucleic acids and polypeptides, useful for diagnosing,

PT treating, preventing or ameliorating diseases or disorders e.g. cancer,
PT anemia, arthritis, asthma, inflammatory bowel disease or Alzheimer's
PT disease.
XX
PS Disclosure; SEQ ID NO 498; 286pp; English.
XX
CC This invention relates to novel polynucleotides encoding human secreted
CC proteins. Specifically, it refers to the vectors, host cells, recombinant
CC and synthetic methods for producing human polynucleotides, polypeptides
CC and antibodies. Furthermore, it relates to screening methods to identify
CC agonists and antagonists that can be used to inhibit or enhance the
CC production and function of the secreted proteins. The present invention
CC describes these compositions as useful for diagnosing, treating or
CC preventing disorders such as cancer, haematopoietic diseases including
CC anaemia and multiple myeloma, reproductive system disorders including
CC prostatitis and inguinal hernia, musculoskeletal diseases including
CC systemic lupus erythematosus and gout, cardiovascular disease including
CC arrhythmia and hypernatraemia, mixed fetal diseases including fetal
CC alcohol syndrome and Down's syndrome, excretory diseases including
CC urinary incontinence and renal disorders, neural or sensory disease
CC including Alzheimer's disease and meningitis, respiratory disease
CC including emphysema and occupational lung disease, endocrine diseases
CC including diabetes and glomerulonephritis, digestive diseases including
CC portal hypertension and irritable bowel syndrome and connective tissue or
CC epithelial diseases including scleroderma and epidermolysis bullosa. As
CC such, there are various activites such as cytostatic, antianemic,
CC antiarthritic, antiasthmatic, anti-HIV, immunosuppressive,
CC antiinflammatory, antipsoriatic, antibacterial, osteopathic,
CC dermatological, antigout, immunomodulator, antiarrhythmic, cardiant,
CC nootropic, antilipemic, nephrotropic, uropathic, neuroprotective,
CC antiparkinsonian, tranquilizer, antidiabetic, anabolic, hypertensive and
CC vulnerary. This polynucleotide is a DNA fragment of a BAC clone that
CC encodes a human secreted protein of the invention. NOTE: This sequence
CC does not appear in the printed specification but has been obtained in
CC electronic format from the US patent office at the following web site
CC www.seqdata.uspto.gov/sequence.html; Document ID: 20040010132.
XX
SQ Sequence 32844 BP; 11125 A; 6089 C; 5587 G; 10043 T; 0 U; 0 Other;

Query Match 2.7%; Score 75; DB 12; Length 32844;
Best Local Similarity 65.9%; Pred. No. 1.3e-08;
Matches 147; Conservative 0; Mismatches 60; Indels 16; Gaps 2;

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Qy       1073 GTATTTTGGATTTTATCAATTTAAAAATTGTGGAAATTTGTTTGCTCTTACGC------- 1125
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Qy       1126 -------CAACATAATATTGATTTTGCCTCTTGGCTCTGAAAGCCCAAAATATTTACCGT 1178
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Qy       1179 CTAGCCCGTTACAGAAAAAGTCTGCTGACTACTGAGCCAGACC 1221
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Job time : 1294 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: November 29, 2004, 08:42:07 ; Search time 11585 Seconds
(without alignments)
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Title: US-09-989-920-100
Perfect score: 2754
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	2754	100.0	2754	6	AX535073	AX535073 Sequence
c	2	2718.4	98.7	211305	9	AC079988	AC079988 Homo sapi
c	3	2718.4	98.7	225203	2	AC140107	AC140107 Homo sapi
c	4	2397.4	87.1	2399	6	AX535064	AX535064 Sequence
	5	1747.6	63.5	1853	6	AR204690	AR204690 Sequence
c	6	820.6	29.8	88036	2	AC139359	AC139359 Homo sapi
	7	803	29.2	88036	2	AC139359	AC139359 Homo sapi
	8	612.4	22.2	960	6	AX535072	AX535072 Sequence
	9	554	20.1	611	6	CQ522682	CQ522682 Sequence
	10	357.4	13.0	395	6	AX262096	AX262096 Sequence
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	17	80.6	2.9	188789	2	AP001446	AP001446 Homo sapi
	18	80.6	2.9	211466	9	AC012301	AC012301 Homo sapi
c	19	77	2.8	175762	2	AC009761	AC009761 Homo sapi
	20	77	2.8	180760	2	AC130435	AC130435 Homo sapi
c	21	77	2.8	194955	9	AC084198	AC084198 Homo sapi
	22	76.6	2.8	736	6	BD274467	BD274467 Cell diff
c	23	76.2	2.8	155301	9	AC041040	AC041040 Homo sapi
	24	75.4	2.7	151687	2	AL356979	AL356979 Homo sapi
	25	75.4	2.7	182529	9	AC092813	AC092813 Homo sapi
c	26	75.4	2.7	202402	2	AC012517	AC012517 Homo sapi
	27	75	2.7	65543	2	AC027356	AC027356 Homo sapi
c	28	75	2.7	126882	9	HS273N12	AL022395 Human DNA
c	29	74.2	2.7	181504	2	AC150610	AC150610 Callithri
	30	73.2	2.7	125066	9	AC074286	AC074286 Homo sapi
c	31	72.4	2.6	137658	9	HS1022J11	AL049765 Human DNA
c	32	72.4	2.6	202157	4	AC124907	AC124907 Equus cab
	33	71.6	2.6	56748	9	AL356852	AL356852 Human DNA
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c	36	70.8	2.6	123395	9	HS889N15	AL031177 Human DNA
c	37	70.2	2.5	195634	2	AC150472	AC150472 Papio anu
c	38	70	2.5	170695	9	AC016134	AC016134 Homo sapi
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c	41	68.8	2.5	34744	9	AL589842	AL589842 Human DNA
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c	43	68.6	2.5	115396	9	AC010366	AC010366 Homo sapi
c	44	68.6	2.5	130530	9	AF131217	AF131217 Homo sapi
c	45	68.6	2.5	168991	2	AC025462	AC025462 Homo sapi

ALIGNMENTS

RESULT 1
AX535073
LOCUS AX535073 2754 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 100 from Patent WO02068633.
ACCESSION AX535073
VERSION AX535073.1 GI:25261753
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Macina,R.A., Recipon,H., Chen,S.Y., Sun,Y. and Liu,C.
TITLE Compositions and methods relating to lung specific genes and proteins
JOURNAL Patent: WO 02068633-A 100 06-SEP-2002;
Diadexus, Inc. (US)
FEATURES Location/Qualifiers
source 1. .2754
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ORIGIN

Query Match 100.0%; Score 2754; DB 6; Length 2754;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2754; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 GCCAGAAGCAGCCTCAGCTTGGCAAGGTGTGGAGATGACTGCTGTTCCCTTCGCATTTGG 60

Qy         61 GGAAAACAGGCTCCCTCGGTAGCTCGATGATCCTCTTTTGATCTTGTGTGACCTCCTGGA 120
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Qy        121 GAGTGGATGACGCTGGTGGCCTTAGCTTTTCTAGACAGTGTAAATTGCACTGGGCGATGT 180
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Qy        181 CCCCAGAGCAGGGCAAGGTCTCTAGAGCGGGTCTCCCACATGACTGGCTTCACACAGGCA 240
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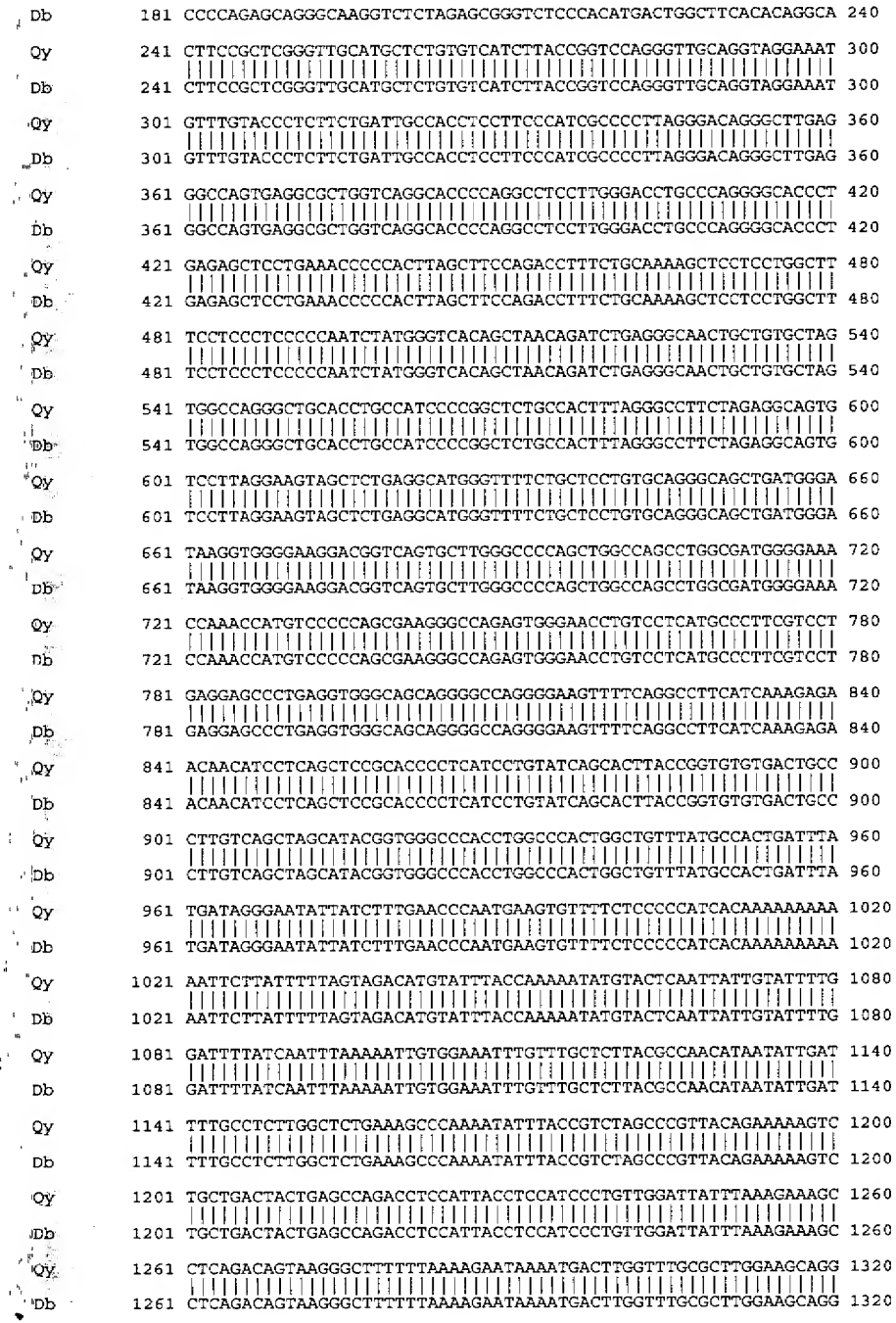

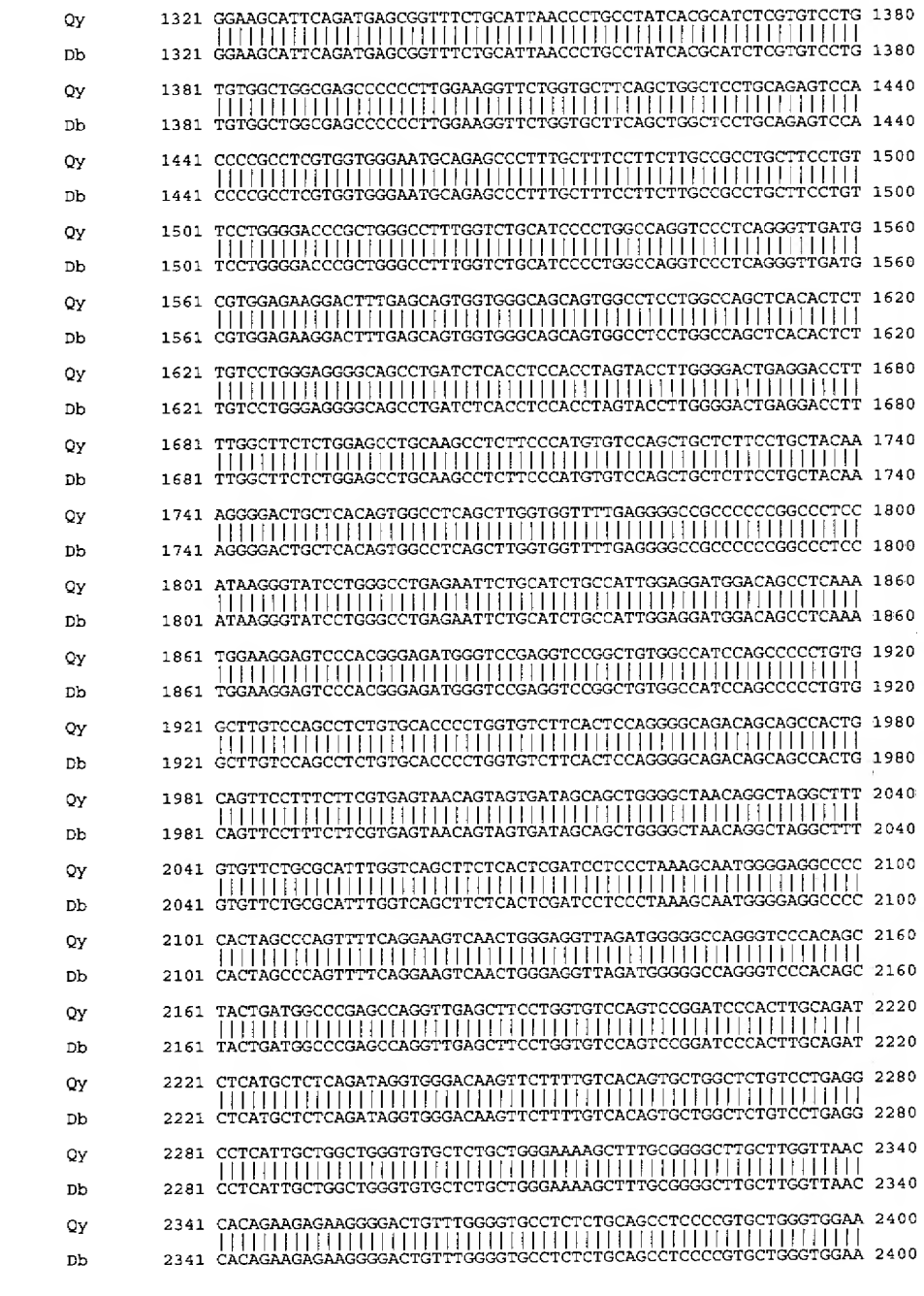

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Db       2401 GCACGGTTACTGTGTTCTCTAATGTTCATGTATTTAAAATGATTTCTTTCTAAAGATGTA 2460

Qy       2461 ACCTCCACACCTTTCTCCAGATTGGGTGACTCTTTTCTAAAGGTGGTGGGAGTATCTGTC 2520
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Db       2461 ACCTCCACACCTTTCTCCAGATTGGGTGACTCTTTTCTAAAGGTGGTGGGAGTATCTGTC 2520

Qy       2521 GGGGTGGTGTGGCCCTTGGATGGGTCAGGTGGGTGTGAGAGGTCCTGGGGAGGTGGGCGT 2580
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Qy       2581 TGAGCTCAAAGTTGTCCTACTGCCATGTTTTTGTACCTGAAATAAAGCATATTTTGCACT 2640
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Qy       2641 TGTTACTGTACCATAGTGCGGACGAGAAGTCTGTATGTGGGATCTGTGCTTGGGTTAGAA 2700
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Db       2641 TGTTACTGTACCATAGTGCGGACGAGAAGTCTGTATGTGGGATCTGTGCTTGGGTTAGAA 2700

Qy       2701 TGCAAATAAAACTCACATTTGTAAGAAAAAAAAAAAAAAATAAAAAGATGCGGCC 2754
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Db       2701 TGCAAATAAAACTCACATTTGTAAGAAAAAAAAAAAAAAATAAAAAGATGCGGCC 2754
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RESULT 2
AC079988/c
LOCUS AC079988 211305 bp DNA linear PRI 09-MAR-2002
DEFINITION Homo sapiens BAC clone RP11-795C1 from 2, complete sequence.
ACCESSION AC079988
VERSION AC079988.6 GI:18873965
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 211305)
AUTHORS Sulston,J.E. and Waterston,R.
TITLE Toward a complete human genome sequence
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE 99063792
PUBMED 9847074
REFERENCE 2 (bases 1 to 211305)
AUTHORS Waligorski,J., Haakenson,W. and Boyer,E.
TITLE The sequence of Homo sapiens BAC clone RP11-795C1
JOURNAL Unpublished (2001)
REFERENCE 3 (bases 1 to 211305)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (20-SEP-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE 4 (bases 1 to 211305)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (23-FEB-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE 5 (bases 1 to 211305)
AUTHORS Waterston,R.
TITLE Direct Submission
JOURNAL Submitted (09-MAR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT On Feb 23, 2002 this sequence version replaced gi:18042517.
---------- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
---------- Summary Statistics
Center project name: H_NH0795C01
----------.

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:
The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa,K., Woon,P.Y., Zhao,B., Frengen,E., Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-60M20, 2000 bp overlap. Actual start of this clone is at base position 1 of RP11-795C1; actual end is at base position 111002 of RP11-69O6.

Single plasmid region exists between 76851 and 76869. Polymorphisms exists between AC067960, AC013399 and AC079988. Data from AC067960 and AC013399 was used to finish AC079988.

FEATURES Location/Qualifiers
source 1. .211305
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Qy        601 TCCTTAGGAAGTAGCTCTGAGGCATGGGTTTTCTGCTCCTGTGCAGGGCAGCTGATGGGA 660
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Qy       1921 GCTTGTCCAGCCTCTGTGCACCCCTGGTGTCTTCACTCCAGGGGCAGACAGCAGCCACTG 1980
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RESULT 3
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LOCUS       AC140107              225203 bp    DNA     linear   HTG 21-FEB-2003
DEFINITION  Homo sapiens chromosome 17 clone RP11-1201C10 map 17, WORKING DRAFT
            SEQUENCE, 4 unordered pieces.
ACCESSION   AC140107
VERSION     AC140107.1  GI:28460978
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 225203)
  AUTHORS   Birren,B., Nusbaum,C. and Lander,E.
  TITLE     Homo sapiens chromosome 17, clone RP11-1201C10
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 225203)
  AUTHORS   Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
            Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
            Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y.,
            Collymore,A., Cook,A., Cooke,P., Corum,B., DeArellano,K.,
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            Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
            Wyman,D., Young,G., Zaincun,J., Zembek,L., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-FEB-2003) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            -------------- Genome Center
                Center: Whitehead Institute/ MIT Center for Genome Research
                Center code: WIBR
                Web site: http://www-seq.wi.mit.edu
                Contact: sequence_submissions@genome.wi.mit.edu
            -------------- Project Information
                Center project name: L29363
                Center clone name: 1201_C_10
            -------------- Summary Statistics
                Sequencing vector: Plasmid; n/a; 100% of reads
                Chemistry: Dye-terminator Big Dye; 100% of reads
                Assembly program: Phrap; version 0.960731
                Consensus quality: 223547 bases at least Q40
                Consensus quality: 224174 bases at least Q30
                Consensus quality: 224530 bases at least Q20
                Insert size: 221000; agarose-fp
                Insert size: 224903; sum-of-contigs
                Quality coverage: 14.9 in Q20 bases; agarose-fp
                Quality coverage: 14.6 in Q20 bases; sum-of-contigs
            --------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 4 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1    46920: contig of 46920 bp in length
            *    46921    47020: gap of 100 bp
            *    47021    51090: contig of 4070 bp in length
            *    51091    51190: gap of 100 bp
            *    51191   163725: contig of 112535 bp in length
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ORIGIN

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  Matches 2722;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

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Qy         61 GGAAAACAGGCTCCCTCGGTAGCTCGATGATCCTCTTTTGATCTTGTGTGACCTCCTGGA 120
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Qy        121 GAGTGGATGACGCTGGTGGCCTTAGCTTTTCTAGACAGTGTAAATTGCACTGGGCGATGT 180
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Qy        181 CCCCAGAGCAGGGCAAGGTCTCTAGAGCGGGTCTCCCACATGACTGGCTTCACACAGGCA 240
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Qy        481 TCCTCCCTCCCCCAATCTATGGGTCACAGCTAACAGATCTGAGGGCAACTGCTGTGCTAG 540
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DEFINITION  Sequence 91 from Patent WO02068633.
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VERSION     AX535064.1  GI:25261735
KEYWORDS    .
SOURCE      Homo sapiens (human)
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REFERENCE   1
  AUTHORS   Macina,R.A., Recipon,H., Chen,S.Y., Sun,Y. and Liu,C.
  TITLE     Compositions and methods relating to lung specific genes and
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ORIGIN
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Query Match 87.1%; Score 2397.4; DB 6; Length 2399;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2398; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      2399 TTGAGGGCCAGTGAGGTGCTGGTCAGGCACCCCAGGCCTCCTTGGGACCTGCCCAGGGGC 2340

Qy       416 ACCCTGAGAGCTCCTGAAACCCCCACTTAGCTTCCAGACCTTTCTGCAAAAGCTCCTCCT 475
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RESULT 5
AR204690
LOCUS       AR204690                1853 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 3 from patent US 6368794.
ACCESSION   AR204690
VERSION     AR204690.1  GI:21502081
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1853)
  AUTHORS   Daniel,S., Gilmore,J., Stuart,S.G. and Stuve,L.L.
  TITLE     Detection of altered expression of genes regulating cell
            proliferation
  JOURNAL   Patent: US 6368794-A 3 09-APR-2002;
FEATURES             Location/Qualifiers
     source          1..1853
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             63.5%;  Score 1747.6;  DB 6;  Length 1853;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1750;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          994 TGTTTTCTCCCCCATCACAAAAAAAAAAATTCTTATTTTTAGTAGACATGTATTTACCAA 1053
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Db            1 TGTTTTCTCCCCCATCACAAAAAAAAAAATTCTTATTTTTAGTAGACATGTATTTACCAA 60

Qy         1054 AAATATGTACTCAATTATTGTATTTTGGATTTTATCAATTTAAAAATTGTGGAAATTTGT 1113
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Db           61 AAATATGTACTCAATTATTGTATTTTGGATTTTATCAATTTAAAAATTGTGGAAATTTGT 120

Qy         1114 TTGCTCTTACGCCAACATAATATTGATTTTGCCTCTTGGCTCTGAAAGCCCAAAATATTT 1173
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Db          121 TTGCTCTTACGCCAACATAATATTGATTTTGCCTCTTGGCTCTGAAAGCCCAAAATATTT 180

Qy         1174 ACCGTCTAGCCCGTTACAGAAAAAGTCTGCTGACTACTGAGCCAGACCTCCATTACCTCC 1233
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Db          181 ACCGTCTAGCCCGTTACAGAAAAAGTCTGCTGACTACTGAGCCAGACCTCCATTACCTCC 240

Qy         1234 ATCCCTGTTGGATTATTTAAAGAAAGCCTCAGACAGTAAGGGCTTTTTAAAAGAATAAA 1293
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Db          241 ATCCCTGTTGGATTATTTAAAGAAAGCCTCAGACAGTAAGGGCTTTTTAAAAGAATAAA 300

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Db          301 ATGACTTGGTTTGCGCTTGGAAGCAGGGGAAGCATTCAGATGAGCGGTTTCTGCATTAAC 360

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Qy         1414 TGCTTCAGCTGGCTCCTGCAGAGTCCACCCCGCCTCGTGGTGGGAATGCAGAGCCCTTTG 1473
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Qy         1654 CCTAGTACCTTGGGGACTGAGGACCTTTTGGCTTCTCTGGAGCCTGCAAGCCTCTTCCCA 1713
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Qy         1714 TGTGTCCAGCTGCTCTTCCTGCTACAAAGGGGACTGCTCACAGTGGCCTCAGCTTGGTGG 1773
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Db          721 TGTGTCCAGCTGCTCTTCCTGCTACAAAGGGGACTGCTCACAGTGGCCTCAGCTTGGTGG 780

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Qy         1834 TGCCATTGGAGGATGGACAGCCTCAAATGGAAGGAGTCCCACGGGAGATGGGTCCGAGGT 1893
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Qy         1894 CCGGCTGTGGCCATCCAGCCCCCTGTGGCTTGTCCAGCCTCTGTGCACCCCTGGTGTCTT 1953
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          901 CCGGCTGTGGCCATCCAGCCCCCTGTGGCTTGTCCAGCCTCTGTGCACCCCTGGTGTCTT 960

Qy         1954 CACTCCAGGGGCAGACAGCAGCCACTGCAGTTCCTTTCTTCGTGAGTAACAGTAGTGATA 2013
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Db          961 CACTCCAGGGGCAGACAGCAGCCACTGCAGTTCCTTTCTTCGTGAGTAACAGTAGTGATA 1020

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Qy         2074 TCCTCCCTAAAGCAATGGGGAGGCCCCCACTAGCCCAGTTTTCAGGAAGTCAACTGGGAG 2133
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Qy         2134 GTTAGATGGGGGCCAGGGTCCCACAGCTACTGATGGCCCGAGCCAGGTTGAGCTTCCTGG 2193
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Qy         2194 TGTCCAGTCCGGATCCCACTTGCAGATCTCATGCTCTCAGATAGGTGGGACAAGTTCTTT 2253
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RESULT 6
AC139359/c
LOCUS       AC139359               88036 bp    DNA     linear   HTG 01-FEB-2003
DEFINITION  Homo sapiens chromosome 17 clone RP11-1162K6 map 17, LOW-PASS
            SEQUENCE SAMPLING.
ACCESSION   AC139359
VERSION     AC139359.1  GI:28191551
KEYWORDS    HTG; HTGS_PHASE0.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 88036)
  AUTHORS   Birren,B., Nusbaum,C. and Lander,E.
  TITLE     Homo sapiens chromosome 17, clone RP11-1162K6
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 88036)
  AUTHORS   Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
            Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
            Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y.,
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            Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M.,
            Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
            Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-FEB-2003) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            -------------- Genome Center
                Center: Whitehead Institute/ MIT Center for Genome Research
                Center code: WIBR
                Web site: http://www-seq.wi.mit.edu
                Contact: sequence_submissions@genome.wi.mit.edu
            -------------- Project Information
                Center project name: L29391
                Center clone name: 1162_K_6
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            * NOTE: This record contains 94 individual
            * sequencing reads that have not been assembled into
            * contigs. Runs of N are used to separate the reads
            * and the order in which they appear is completely
            * arbitrary. Low-pass sequence sampling is useful for
            * identifying clones that may be gene-rich and allows
            * overlap relationships among clones to be deduced.
            * However, it should not be assumed that this clone
            * will be sequenced to completion. In the event that
            * the record is updated, the accession number will
            * be preserved.
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            *    17741    18591: contig of 851 bp in length
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            *    19642    20489: contig of 848 bp in length
            *    20490    20589: gap of 100 bp
            *    20590    21422: contig of 833 bp in length
            *    21423    21522: gap of 100 bp
            *    21523    22357: contig of 835 bp in length
            *    22358    22457: gap of 100 bp
            *    22458    23292: contig of 835 bp in length
            *    23293    23392: gap of 100 bp
            *    23393    24230: contig of 838 bp in length
            *    24231    24330: gap of 100 bp
            *    24331    25143: contig of 813 bp in length
            *    25144    25243: gap of 100 bp
            *    25244    26055: contig of 812 bp in length
            *    26056    26155: gap of 100 bp
            *    26156    27000: contig of 845 bp in length
            *    27001    27100: gap of 100 bp
            *    27101    27947: contig of 847 bp in length
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*    32776    33614: contig of 839 bp in length
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*    43127    44011: contig of 885 bp in length
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*    45982    46811: contig of 830 bp in length
*    46812    46911: gap of 100 bp
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*    50522    50621: gap of 100 bp
*    50622    51478: contig of 857 bp in length
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*    54335    54434: gap of 100 bp
*    54435    55273: contig of 839 bp in length
*    55274    55373: gap of 100 bp
*    55374    56210: contig of 837 bp in length
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*    56311    57148: contig of 838 bp in length
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*    58180    59004: contig of 825 bp in length
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*    62836    63686: contig of 851 bp in length
*    63687    63786: gap of 100 bp
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  Query Match             29.8%;  Score 820.6;  DB 2;  Length 88036;
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  Matches  838;  Conservative    0;  Mismatches  238;  Indels    0;  Gaps    0;

Qy       427 TCCTGAAACCCCCACTTAGCTTCCAGACCTTTCTGCAAAAGCTCCTCCTGGCTTTCCTCC 486
            |
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Qy       487 CTCCCCCAATCTATGGGTCACAGCTAACAGATCTGAGGGCAACTGCTGTGCTAGTGGCCA 546
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Db     73067 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGCTGTGCTAGTGGCCA 73008

Qy       547 GGGCTGCACCTGCCATCCCCGGCTCTGCCACTTTAGGGCCTTCTAGAGGCAGTGTCCTTA 606
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Qy       607 GGAAGTAGCTCTGAGGCATGGGTTTTCTGCTCCTGTGCAGGGCAGCTGATGGGATAAGGT 666
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Db     72947 GGAAGTAGCTCTGAGGCATGGGTTTTCTGCTCCTGTGCAGGGCAGCTGATGGGATAAGGT 72888

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Qy       727 CATGTCCCCCAGCGAAGGGCCAGAGTGGGAACCTGTCCTCATGCCCTTCGTCCTGAGGAG 786
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Db     72767 CCCTGAGGTGGGCAGCAGGGGCCAGGGGAAGTTTTCAGGCCTTCATCAAAGAGAACAACA 72708

Qy       847 TCCTCAGCTCCGCACCCCTCATCCTGTATCAGCACTTACCGGTGTGTGACTGCCCTTGTC 906
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Db     72707 TCCTCAGCTCCGCACCCCTCATCCTGTATCAGCACTTACCGGTGTGTGACTGCCCTTGTC 72648

Qy       907 AGCTAGCATACGGTGGGCCCACCTGGCCCACTGGCTGTTTATGCCACTGATTTATGATAG 966
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Db     72647 AGCTAGCATACGGTGGGCCCACCTGGCCCACTGGCTGTTTATGCCACTGATTTATGATAG 72588

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Db     72407 TCTTGGCTCTGAAAGCCCAAAATATTTACCGTCTAGCCCGTTACAGAAAAAGTCTGCTGA 72348

Qy      1207 CTACTGAGCCAGACCTCCATTACCTCCATCCCTGTTGGATTATTTAAAGAAAGCCTCAGA 1266
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     72347 CTACTGAGCCAGACCTCCATTACCTCCATCCCTGTTGGATTATTTAAAGAAAGCCTCAGA 72288

Qy      1267 CAGTAAGGGCTTTTTTAAAAGAATAAAATGACTTGGTTTGCGCTTGGAAGCAGGGGAAGC 1326
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     72287 CAGTAAGGGCTTTTTTAAAAGAATAAAATGACTTGGTTTGCGCTTGGAAGCAGGGGAAGC 72228

Qy      1327 ATTCAGATGAGCGGTTTCTGCATTAACCCTGCCTATCACGCATCTCGTGTCCTGTGTGGC 1386
            |||||||||||||||||| |||   |  |  |  |  |||| |
Db     72227 ATTCAGATGAGCGGTTTCTGAATTCCANCCCCAGGGCGAGATCATCGTTTNNNNNNNNNN 72168

Qy      1387 TGGCGAGCCCCCCTTGGAAGGTTCTGGTGCTTCAGCTGGCTCCTGCAGAGTCCACCCCGC 1446
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Db      72167 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 72108

Qy       1447 CTCGTGGTGGGAATGCAGAGCCCTTTGCTTTCCTTCTTGCCGCCTGCTTCCTGTTC 1502
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Db      72107 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNTTCTATACTTTATTCTGTTTC 72052

RESULT 7
AC139359
LOCUS       AC139359              88036 bp    DNA     linear   HTG 01-FEB-2003
DEFINITION  Homo sapiens chromosome 17 clone RP11-1162K6 map 17, LOW-PASS
            SEQUENCE SAMPLING.
ACCESSION   AC139359
VERSION     AC139359.1  GI:28191551
KEYWORDS    HTG; HTGS_PHASE0.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 88036)
  AUTHORS   Birren,B., Nusbaum,C. and Lander,E.
  TITLE     Homo sapiens chromosome 17, clone RP11-1162K6
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 88036)
  AUTHORS   Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
            Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
            Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y.,
            Collymore,A., Cook,A., Cooke,P., Corum,B., DeArellano,K.,
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            Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,
            Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J.,
            Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,
            O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
            Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,
            Roman,J., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C.,
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            Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M.,
            Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
            Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-FEB-2003) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            -------------- Genome Center
                Center: Whitehead Institute/ MIT Center for Genome Research
                Center code: WIBR
                Web site: http://www-seq.wi.mit.edu
                Contact: sequence_submissions@genome.wi.mit.edu
            -------------- Project Information
                Center project name: L29391
                Center clone name: 1162_K_6
            --------------.
            * NOTE: This record contains 94 individual
            * sequencing reads that have not been assembled into
            * contigs. Runs of N are used to separate the reads
            * and the order in which they appear is completely
            * arbitrary. Low-pass sequence sampling is useful for
            * identifying clones that may be gene-rich and allows
            * overlap relationships among clones to be deduced.
            * However, it should not be assumed that this clone
            * will be sequenced to completion. In the event that
            * the record is updated, the accession number will
            * be preserved.
            *        1      856: contig of 856 bp in length
            *      857      956: gap of 100 bp
            *      957     1784: contig of 828 bp in length
            *     1785     1884: gap of 100 bp
            *     1885     2709: contig of 825 bp in length
            *     2710     2809: gap of 100 bp
            *     2810     3605: contig of 796 bp in length
            *     3606     3705: gap of 100 bp
            *     3706     4555: contig of 850 bp in length
            *     4556     4655: gap of 100 bp
            *     4656     5496: contig of 841 bp in length
            *     5497     5596: gap of 100 bp
            *     5597     6438: contig of 842 bp in length
            *     6439     6538: gap of 100 bp
            *     6539     7389: contig of 851 bp in length
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            *     7490     8316: contig of 827 bp in length
            *     8317     8416: gap of 100 bp
            *     8417     9255: contig of 839 bp in length
            *     9256     9355: gap of 100 bp
            *     9356    10180: contig of 825 bp in length
            *    10181    10280: gap of 100 bp
            *    10281    11109: contig of 829 bp in length
            *    11110    11209: gap of 100 bp
            *    11210    12059: contig of 850 bp in length
            *    12060    12159: gap of 100 bp
            *    12160    12982: contig of 823 bp in length
            *    12983    13082: gap of 100 bp
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            *    13995    14795: contig of 801 bp in length
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            *    14896    15736: contig of 841 bp in length
            *    15737    15836: gap of 100 bp
            *    15837    16691: contig of 855 bp in length
            *    16692    16791: gap of 100 bp
            *    16792    17640: contig of 849 bp in length
            *    17641    17740: gap of 100 bp
            *    17741    18591: contig of 851 bp in length
            *    18592    18691: gap of 100 bp
            *    18692    19541: contig of 850 bp in length
            *    19542    19641: gap of 100 bp
            *    19642    20489: contig of 848 bp in length
            *    20490    20589: gap of 100 bp
            *    20590    21422: contig of 833 bp in length
            *    21423    21522: gap of 100 bp
            *    21523    22357: contig of 835 bp in length
            *    22358    22457: gap of 100 bp
            *    22458    23292: contig of 835 bp in length
            *    23293    23392: gap of 100 bp
            *    23393    24230: contig of 838 bp in length
            *    24231    24330: gap of 100 bp
            *    24331    25143: contig of 813 bp in length
            *    25144    25243: gap of 100 bp
            *    25244    26055: contig of 812 bp in length
            *    26056    26155: gap of 100 bp
            *    26156    27000: contig of 845 bp in length
            *    27001    27100: gap of 100 bp
            *    27101    27947: contig of 847 bp in length
            *    27948    28047: gap of 100 bp
            *    28048    28896: contig of 849 bp in length
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            *    28997    29847: contig of 851 bp in length
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            *    30884    31729: contig of 846 bp in length
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            *    34660    35489: contig of 830 bp in length
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*    35490    35589: gap of 100 bp
*    35590    36408: contig of 819 bp in length
*    36409    36508: gap of 100 bp
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*    37316    37415: gap of 100 bp
*    37416    38262: contig of 847 bp in length
*    38263    38362: gap of 100 bp
*    38363    39213: contig of 851 bp in length
*    39214    39313: gap of 100 bp
*    39314    40166: contig of 853 bp in length
*    40167    40266: gap of 100 bp
*    40267    41123: contig of 857 bp in length
*    41124    41223: gap of 100 bp
*    41224    42077: contig of 854 bp in length
*    42078    42177: gap of 100 bp
*    42178    43026: contig of 849 bp in length
*    43027    43126: gap of 100 bp
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*    44112    44943: contig of 832 bp in length
*    44944    45043: gap of 100 bp
*    45044    45881: contig of 838 bp in length
*    45882    45981: gap of 100 bp
*    45982    46811: contig of 830 bp in length
*    46812    46911: gap of 100 bp
*    46912    47727: contig of 816 bp in length
*    47728    47827: gap of 100 bp
*    47828    48636: contig of 809 bp in length
*    48637    48736: gap of 100 bp
*    48737    49571: contig of 835 bp in length
*    49572    49671: gap of 100 bp
*    49672    50521: contig of 850 bp in length
*    50522    50621: gap of 100 bp
*    50622    51478: contig of 857 bp in length
*    51479    51578: gap of 100 bp
*    51579    52428: contig of 850 bp in length
*    52429    52528: gap of 100 bp
*    52529    53390: contig of 862 bp in length
*    53391    53490: gap of 100 bp
*    53491    54334: contig of 844 bp in length
*    54335    54434: gap of 100 bp
*    54435    55273: contig of 839 bp in length
*    55274    55373: gap of 100 bp
*    55374    56210: contig of 837 bp in length
*    56211    56310: gap of 100 bp
*    56311    57148: contig of 838 bp in length
*    57149    57248: gap of 100 bp
*    57249    58079: contig of 831 bp in length
*    58080    58179: gap of 100 bp
*    58180    59004: contig of 825 bp in length
*    59005    59104: gap of 100 bp
*    59105    59910: contig of 806 bp in length
*    59911    60010: gap of 100 bp
*    60011    60839: contig of 829 bp in length
*    60840    60939: gap of 100 bp
*    60940    61784: contig of 845 bp in length
*    61785    61884: gap of 100 bp
*    61885    62735: contig of 851 bp in length
*    62736    62835: gap of 100 bp
*    62836    63686: contig of 851 bp in length
*    63687    63786: gap of 100 bp
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Query Match             29.2%;  Score 803;  DB 2;  Length 88036;
Best Local Similarity   100.0%;  Pred. No. 1.9e-188;
Matches  803;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        861 CCCCTCATCCTGTATCAGCACTTACCGGTGTGTGACTGCCCTTGTCAGCTAGCATACGGT 920
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Db      82558 CCCCTCATCCTGTATCAGCACTTACCGGTGTGTGACTGCCCTTGTCAGCTAGCATACGGT 82617

Qy        921 GGGCCCACCTGGCCCACTGGCTGTTTATGCCACTGATTTATGATAGGGAATATTATCTTT 980
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Db      82618 GGGCCCACCTGGCCCACTGGCTGTTTATGCCACTGATTTATGATAGGGAATATTATCTTT 82677

Qy        981 GAACCCAATGAAGTGTTTTCTCCCCCATCACAAAAAAAAAAAATTCTTATTTTTAGTAGAC 1040
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Qy       1041 ATGTATTTACCAAAAATATGTACTCAATTATTGTATTTTGGATTTTATCAATTTAAAAAT 1100
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Qy       1101 TGTGGAAATTTGTTTGCTCTTACGCCAACATAATATTGATTTTGCCTCTTGGCTCTGAAA 1160
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Qy       1161 GCCCAAAATATTTACCGTCTAGCCCGTTACAGAAAAAGTCTGCTGACTACTGAGCCAGAC 1220
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Qy       1281 TTAAAAGAATAAAATGACTTGGTTTGCGCTTGGAAGCAGGGGAAGCATTCAGATGAGCGG 1340
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Db      82978 TTAAAAGAATAAAATGACTTGGTTTGCGCTTGGAAGCAGGGGAAGCATTCAGATGAGCGG 83037

Qy       1341 TTTCTGCATTAACCCTGCCTATCACGCATCTCGTGTCCTGTGTGGCTGGCGAGCCCCCCT 1400
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Qy       1401 TGGAAGGTTCTGGTGCTTCAGCTGGCTCCTGCAGAGTCCACCCCGCCTCGTGGTGGGAAT 1460
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Qy       1461 GCAGAGCCCTTTGCTTTCCTTCTTGCCGCCTGCTTCCTGTTCCTGGGGACCCGCTGGGCC 1520
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LOCUS       AX535072                960 bp    DNA     linear   PAT 22-NOV-2002
DEFINITION  Sequence 99 from Patent WO02068633.
ACCESSION   AX535072
VERSION     AX535072.1  GI:25261751
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Macina,R.A., Recipon,H., Chen,S.Y., Sun,Y. and Liu,C.
  TITLE     Compositions and methods relating to lung specific genes and
            proteins
  JOURNAL   Patent: WO 02068633-A 99 06-SEP-2002;
            Diadexus, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .960
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/db_xref="taxon:9606"

ORIGIN

Query Match 22.2%; Score 612.4; DB 6; Length 960;
Best Local Similarity 99.4%; Pred. No. 4e-141;
Matches 646; Conservative 0; Mismatches 1; Indels 3; Gaps 3;

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Qy       1718 TCCAGCTGCTCTTCCTGCTACAAAGGGGACTGCTCACAGTGGCCTCAGCTTGGTGGTTTT 1777
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Qy       1778 GAGGGGCCGCCCCCCGGCCCTCCATAAGGGTATCCTGGGCCTGAGAATTCTGCATCTGCC 1837
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Db        161 GAGGGGCCGCCCCCCGGCCCTCCATAAGGGTATCCTGGGCCTGAGAATTCTGCATCTGCC 220

Qy       1838 ATTGGAGGATGGACAGCCTCAAATGGAAGGAGTCCCACGGGAGATGGGTCCGAGGTCCGG 1897
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Db        221 ATTGGAGGATGGACAGCCTCAAATGGAAGGAGTCCCACGGGAGATGGGTCCGAGGTCCGG 280

Qy       1898 CTGTGGCCATCCAGCCCCCTGTGGCTTGTCCAGCCTCTGTGCACCCCTGGTGTCTTCACT 1957
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 CTGTGGCCATCCAGCCCCCTGTGGCTTGTCCAGCCTCTGTGCACCCCTGGTGTCTTCACT 340

Qy       1958 CCAGGGGCAGACAGCAGCCACTGCAGTTCCTTTCTTCGTGAGTAACAGTAGTGATAGCAG 2017
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       2018 CTGGGGCTAACAGGCTAGGCTTTGTGTTCTGCGCATTTGGTCAGCTTCTCACTCGATCCT 2077
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Qy       2078 CCCTAAAGCAATGGGGAGGCCCCCACTAGCCCAGTTTTCAGGAAGTCAACTGGGAGGTTA 2137
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RESULT 9
CQ522682
LOCUS CQ522682 611 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 54549 from Patent WO0160860.
ACCESSION CQ522682
VERSION CQ522682.1 GI:41488946
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Schlegel,R., Endege,W.O. and Monahan,J.E.
TITLE Genes differentially expressed in human prostate cancer and their use
JOURNAL Patent: WO 0160860-A 54549 23-AUG-2001;
Millennium Predictive Medicine, Inc. (US)
FEATURES Location/Qualifiers
source 1. .611
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 20.1%; Score 554; DB 6; Length 611;
Best Local Similarity 99.5%; Pred. No. 1.4e-126;
Matches 565; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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Db         44 AAAAGTCTGCTGACTACTGAGCCAGACCTCCATTACCTCCATCCCTGTTGGATTATTTAA 103

Qy       1254 AGAAAGCCTCAGACAGTAAGGGC-TTTTTTAAAAGAATAAAATGACTTGGTTTGCGCTTG 1312
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Db        104 AGAAAGCCTCAGACAGTAAGGGCTTTTTTTAAAAGAATAAAATGACTTGGTTTGCGCTTG 163

Qy       1313 GAAGCAGGGGAAGCATTCAGATGAGCGGTTTCTGCATTAACCCTGCCTATCACGCATCTC 1372
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Db        164 GAAGCAGGGGAAGCATTCAGATGAGCGGTTTCTGCATTAACCCTGCCTATCACGCATCTC 223

Qy       1373 GTGTCCTGTGTGGCTGGCGAGCCCCCCTTGGAAGGTTCTGGTGCTTCAGCTGGCTCCTGC 1432
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Qy       1433 AGAGTCCACCCCGCCTCGTGGTGGGAATGCAGAGCCCTTTGCTTTCCTTCTTGCCGCCTG 1492
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Qy       1493 CTTCCTGTTCCTGGGGACCCGCTGGGCCTTTGGTCTGCATCCCCTGGCCAGGTCCCTCAG 1552
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Db        344 CTTCCTGTTCCTGGGGACCCGCTGGGCCTTTGGTCTGCATCCCCTGGCCAGGTCCCTCAG 403

Qy       1553 GGTTGATGCGTGGAGAAGGACTTTGAGCAGTGGTGGGCAGCAGTGGCCTCCTGGCCAGCT 1612
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Db        404 GGTTGATGCGTGGAGAAGGACTTTGAGCAGTGGTGGGCAGCAGTGGCCTCCTGGCCAGCT 463

Qy       1613 CACACTCTTGTCCTGGGAGGGGCAGCCTGATCTCACCTCCACCTAGTACCTTGGGGACTG 1672
             |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        464 CACACTCTTGTCCTGNGAGGGGCAGCCTGATCTCACCTCCACCTAGTACCTTGGGGACTG 523

Qy       1673 AGGACCTTTTGGCTTCTCTGGAGCCTGCAAGCCTCTTCCCATGTGTCCAGCTGCTCTTCC 1732
             |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        524 AGGACCTTTTGGCTTCTCTGGAGCCTGCAAGCCTCTTCCCATGTGTNCAGCTGCTCTTCC 583

Qy       1733 TGCTACAAAGGGGACTGCTCACAGTGGC 1760
             ||||||||||||||||||||||||||||
Db        584 TGCTACAAAGGGGACTGCTCACAGTGGC 611
```

RESULT 10
AX262096
LOCUS AX262096 395 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 176 from Patent WO0172781.
ACCESSION AX262096
VERSION AX262096.1 GI:16511048
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Williams,L.T., Escobedo,J., Innis,M.A., Garcia,P.D.,
Sudduth-Klinger,J., Reinhard,C., He,Z., Randazzo,F., Kennedy,G.C.,
Pot,D., Kassam,A., Lamson,G., Drmanac,R., Crkvenjakov,R.,
Dickson,M., Drmanac,S., Labat,I., Leshkowitz,D., Kita,D.,
Garcia,V., Jones,L.W. and Stache-Crain,B.
JOURNAL Patent: WO 0172781-A 176 04-OCT-2001;
Chiron Corporation (US) ; Hyseq Inc. (US)
FEATURES Location/Qualifiers
source 1. .395
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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ORIGIN

  Query Match            13.0%;  Score 357.4;  DB 6;  Length 395;
  Best Local Similarity  96.9%;  Pred. No. 1.2e-77;
  Matches  375;  Conservative    0;  Mismatches   11;  Indels    1;  Gaps    1;

Qy       1216 CAGACCTCCATTACCTCCATCCCTGTTGGATTATTTAAAGAAAGCCTCAGACAGTAAGGG 1275
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          9 CAGACCTCCATTACCTCCATCCCTGTTGGATTATTTAAAGAAAGCCTCAGACAGTAAGGG 68

Qy       1276 C-TTTTTTAAAAGAATAAAATGACTTGGTTTGCGCTTGGAAGCAGGGGAAGCATTCAGAT 1334
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 CTTTTTTTAAAAGAATAAAATGACTTGGTTTGCGCTTGGAAGCAGGGGAAGCATTCAGAT 128

Qy       1335 GAGCGGTTTCTGCATTAACCCTGCCTATCACGCATCTCGTGTCCTGTGTGGCTGGCGAGC 1394
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 GAGCGGTTTCTGCATTAACCCTGCCTATCACGCATCTCGTGTCCTGTGTGGCTGGCGAGC 188

Qy       1395 CCCCCTTGGAAGGTTCTGGTGCTTCAGCTGGCTCCTGCAGAGTCCACCCCGCCTCGTGGT 1454
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 CCCCCTTGGAAGGTTCTGGTGCTTCAGCTGGCTCCTGCAGAGTCCACCCCGCCTCGTGGT 248

Qy       1455 GGGAATGCAGAGCCCTTTGCTTTCCTTCTTGCCGCCTGCTTCCTGTTCCTGGGGACCCGC 1514
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 GGGAATGCAGAGCCCTTTGCTTTCCTTCTTGCCGCCTGCTTCCTGTTCCTGGGGACCCGC 308

Qy       1515 TGGGCCTTTGGTCTGCATCCCCTGGCCAGGTCCCTCAGGGTTGATGCGTGGAGAAGGACT 1574
             |||||||||||||||||||||||||||||||||||| ||||||| | |||||||||
Db        309 TGGGCCTTTGGTCTGCATCCCCTGGCCAGGTCCCTCAGGGCTGATGCGCGTAGAAGGACT 368

Qy       1575 TTGAGCAGTGGTGGGCAGCAGTGGCCT 1601
             ||||||||||||||  || |||
Db        369 TTGAGCAGTGGTGGCAGCACTTGCCCT 395


RESULT 11
G38425/c
LOCUS       G38425                   406 bp    DNA     linear   STS 23-JUN-1998
DEFINITION  SHGC-58087 Human Homo sapiens STS genomic, sequence tagged site.
ACCESSION   G38425
VERSION     G38425.1  GI:3249199
KEYWORDS    STS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 406)
  AUTHORS   Myers,R.M.
  TITLE     Human STSs (1998)
  JOURNAL   Unpublished (1998)
COMMENT
            Contact: Richard M. Myers
            Stanford Human Genome Center (SHGC)
            Stanford University School of Medicine
            Department of Genetics, M-344, Stanford, CA 94305, USA
            Tel: 4157259687
            Fax: 4157259689
            Email: myers@shgc.stanford.edu
            Primer A: AGCTGACAAGGGCAGTCACA
            Primer B: GGGGAAGTTTTCAGGCCTTC
            STS size: 102
            PCR Profile:
                    Initial incubation: 95 degrees C for 10 minutes

                    Denaturation:       94 degrees C for 30 seconds
                    Annealing:          60 degrees C for 30 seconds
                    Polymerization:     72 degrees C for 23 seconds
                    PCR Cycles:         30
                    Thermal Cycler:     Perkin Elmer 9700
            Protocol:
                    Template:                25 ng
                    Primer:                  each 1 uM
                    dNTPs:                   each 200 uM
                    AmpliTaq Gold Polymerase: 0.07 units/ul
                    Total Vol:               5 ul

            Buffer:
                    MgCl2:          2.5 mM
                    KCl:            50 mM
                    Tris-HCl:       10 mM
                    pH:             8.3

            Prepared with primer pairs derived from W86076 -- Unigene.
FEATURES            Location/Qualifiers
     source         1. .406
                    /organism="Homo sapiens"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:9606"
                    /map="2"
                    /clone_lib="Human"
     STS            100. .201
     primer_bind    100. .119
     primer_bind    complement(182. .201)
ORIGIN

  Query Match             9.5%;  Score 261.2;  DB 11;  Length 406;
  Best Local Similarity  89.2%;  Pred. No. 1.1e-53;
  Matches  347;  Conservative    0;  Mismatches   33;  Indels    9;  Gaps    6;

Qy        630 TTTCTGCTCCTGTGCAGGGCAGCTGATGGG-ATAAGGTGGGGAAGGACGG--TCAGTGCT 686
              || || |   ||    || |||||||||| ||||||||||||||||||    |||||||
Db        387 TTNCTCCCTGTGCAAGGGCCAGCTGATGGGNATAAGGTGGGGAAGGACGGGTCCAGTGCT 328

Qy        687 TGGGCCCCAGCTGGCC--AGCCTGGCGATGGGGAAACCAAACCATGTCCCCCAGCGAAGG 744
              ||| ||| ||||| ||    | |  ||||||||||||||||||||||||||||||||||
Db        327 TGGCCCCNAGCTGNCCCAGCCTGGCGGATGGGGAAACCAAACCATGTCCCCCAGCGAAGG 268

Qy        745 GCCAGAGTGGGAACCTGTCCTCATGCCCTTCGTCCTGAGGAGCCCTGAGGTGGGCAGCAG 804
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 GCCAGAGTGGGAACCTGTCCTCATGCCCTTCGTCCTGAGGAGCCCTGAGGTGGGCAGCAG 208

Qy        805 GGGCCAGGGGAAGTTTTCAGGCCTTCATCAAAGAGAACAACATCC-TCAGCTCCGCACCC 863
              |||||||||||||||||||||||||||||||||||||||||||| ||   |||||||||
Db        207 GGGCCAGGGGAAGTTTTCAGGCCTTCATCAAAGAGAACAACATCCGTCGAGTCCGCACCC 148

Qy        864 CTC-ATCCTGTATCAGCACTTACCGGTGTGTGACTGCCCTTGTCAGCTAGCATACGGTGG 922
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||     ||
Db        147 CTCGATCCTGTATCAGCACTTACCGGTGTGTGACTGCCCTTGTCAGCTAGCAT--CACGG 90

Qy        923 GCCCACCTGGCCCACTGGCTGTTTATGCCACTGATTTATGATAGGGAATATTATCTTTGA 982
                ||  |  | ||||||||||||||||||||||||||||||||||||||||||||||||
Db         89 NGCCCACCTGNCCACTGGCTGTTTATGCCACTGATTTATGATAGGGAATATTATCTTTGA 30

Qy        983 ACCCAATGAAGTGTTTTCTCCCCCATCAC 1011
              |||||||||||||||||||||||||||||
Db         29 ACCCAATGAAGTGTTTTCTCCCCCATCAC 1


RESULT 12
AX535063/c
LOCUS       AX535063                 251 bp    DNA     linear   PAT 22-NOV-2002
DEFINITION  Sequence 90 from Patent WO02068633.
ACCESSION   AX535063
VERSION     AX535063.1  GI:25261733
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Macina,R.A., Recipon,H., Chen,S.Y., Sun,Y. and Liu,C.
  TITLE     Compositions and methods relating to lung specific genes and
            proteins
  JOURNAL   Patent: WO 02068633-A 90 06-SEP-2002;
            Diadexus, Inc. (US)
FEATURES            Location/Qualifiers
```

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     source          1. .251
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

 Query Match              8.1%;  Score 224.4;  DB 6;  Length 251;
 Best Local Similarity   98.8%;  Pred. No. 1.6e-44;
 Matches  237;  Conservative    0;  Mismatches    1;  Indels    2;  Gaps    1;

Qy       2381 CCTCCCCGTGCTGGGTGGAAGCACGGTTACTGTGTTCTCTAATGTTCATGTATTTAAAAT 2440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 CCTCCCCGTGCTGGGTGGAAGCACGGTTACTGTGTTCTCTAATGTTCATGTATTTAAAAT 192

Qy       2441 GATTTCTTTCTAAAGATGTAACCTCCACACCTTTCTCCAGATTGGGTGACTCTTTTCTAA 2500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         191 GATTTCTTTCTAAAGATGTAACCTCCACACCTTTCTCCAGATTGGGTGACTCTTTTCTAA 132

Qy       2501 AGGTGGTGGGAGTATCTGTCGGGGTGGTGTGGCCCTTGGATGGGTCAGGTGGGTGTGAGA 2560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         131 AGGTGGTGGGAGTATCTGTCGGGGTGGTGTGGCCCTTGGATGGGTCAGGTGGGTGTGAGA 72

Qy       2561 GGTCCTGGGGAGGT--GGGCGTTGAGCTCAAAGTTGTCCTACTGCCATGTTTTTGTACCT 2618
             |||||||||||||  | ||||||||||||||||||||||||||||||||||||||||||
Db          71 GGTCCTGGGGAGGTGCGCGCGTTGAGCTCAAAGTTGTCCTACTGCCATGTTTTTGTACCT 12


RESULT 13
AC134136/c
LOCUS       AC134136              190379 bp    DNA     linear   HTG 20-NOV-2002
DEFINITION  Rattus norvegicus clone CH230-298J1, *** SEQUENCING IN PROGRESS
            ***, 2 unordered pieces.
ACCESSION   AC134136
VERSION     AC134136.2  GI:25138971
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 190379)
  AUTHORS   Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
            Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
            Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
            Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
            Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
            Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
            Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
            Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
            Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
            Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
            Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
            Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
            Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
            Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
            Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
            Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
            Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
            Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
            Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M.,
            Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A.,
            Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
            Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
            Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
            Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
            Lorensuhewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J.,
            Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A.,
            Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
            Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,
            Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S.,
            Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L.,
            Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
            Nwaokelemeh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K.,
            Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C.,
            Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L.,
            Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,
            Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
            Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,
            Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,
            Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D.,
            Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,
            Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C.,
            Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K.,
            Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J.,
            Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
            Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K.,
            Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
            Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
            Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
            Weinstock,G. and Gibbs,R.A.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 190379)
  AUTHORS   Rat Genome Sequencing Consortium.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-SEP-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
REFERENCE   3  (bases 1 to 190379)
  AUTHORS   Rat Genome Sequencing Consortium.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-NOV-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     On Nov 20, 2002 this sequence version replaced gi:23269326.
            The sequence in this assembly is a combination of BAC based reads
            and whole genome shotgun sequencing reads assembled using Atlas
            (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
            in the feature table below represents a scaffold in the Atlas
            assembly (a 'contig-scaffold'). Within each contig-scaffold,
            individual sequence contigs are ordered and oriented, and separated
            by sized gaps filled with Ns to the estimated size. The sequence
            may extend beyond the ends of the clone and there may be sequence
            contigs within a contig-scaffold that consist entirely of whole
            genome shotgun sequence reads. Both end sequences and whole genome
            shotgun sequence only contigs will be indicated in the feature
            table.
            -------------- Genome Center
                Center: Baylor College of Medicine
                Center code: BCM
                Web site: http://www.hgsc.bcm.tmc.edu/
                Contact: hgsc-help@bcm.tmc.edu
            -------------- Project Information
                Center project name: KCCX
                Center clone name: CH230-298J1
            -------------- Summary Statistics
                Assembly program: Phrap; version 0.990329
                Consensus quality: 168342 bases at least Q40
                Consensus quality: 171971 bases at least Q30
                Consensus quality: 174193 bases at least Q20
                Estimated insert size: 172482; sum-of-contigs estimation
                Quality coverage: 5x in Q20 bases; sum-of-contigs estimation
            --------------
            * NOTE: Estimated insert size may differ from sequence length
            *   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 2 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1    14191: contig of 14191 bp in length
            *    14192    14291: gap of unknown length
            *    14292   190379: contig of 176088 bp in length.
```

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FEATURES             Location/Qualifiers
     source          1. .190379
                     /organism="Rattus norvegicus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10116"
                     /clone="CH230-298J1"
     misc_feature    1. .1314
                     /note="wgs_contig"
     misc_feature    10470. .12661
                     /note="wgs_contig"
     misc_feature    12712. .14191
                     /note="wgs_contig"
     misc_feature    113270. .115130
                     /note="wgs_contig"
     misc_feature    complement(170214. .171114)
                     /note="clone_boundary
                     clone_end:Sp6
                     site:
                     end_sequence:BZ129373"
     misc_feature    186833. .188023
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                     clone_end:Sp6"
     misc_feature    189278. .190379
                     /note="wgs_end_extension
                     clone_end:Sp6"
ORIGIN

  Query Match             3.2%;  Score 87.6;  DB 2;  Length 190379;
  Best Local Similarity   65.6%;  Pred. No. 2.9e-10;
  Matches  269;  Conservative    0;  Mismatches   99;  Indels   42;  Gaps    8;

Qy       2304 CTGCTGGGAAAAGCTTTGCGGGGCTTGCTTGGTTAACCACAGAAGAGAAGGGGACTGTTT 2363
             |||||||| | ||||| | |||||     | ||      | | |||  |||| ||||||||
Db       5492 CTGCTGGGGAGAGCTTAGTGGGGC-----TAGTATCAGAGACAAGCAAAGGAGACTGTTT 5438

Qy       2364 GGGGTGCCTCTCTGCAGCCTCCCCGTGCTGGGTGGAAGCACGGTTACTGTGTTCTCTAAT 2423
                |   | ||      |||  | ||||||||  | ||  |||||||||||||| | ||
Db       5437 CATG---CACTGACTTATCTCTTCCTGCTGGGTAAAGGCTTGGTTACTGTGTTCTTTCAT 5381

Qy       2424 GTTCATGTATTTAAAATGATTTCTTTCTAAAGATGTAACCTCCACACCTTTCTCCAGATT 2483
              | |      |      |||  | ||   | |        |     |  ||| ||| || |
Db       5380 GCTTCGAAGTGATTCCTGAGGTTTTCTCACA--------CCTACCTTCTTCCTCTAGGTG 5329

Qy       2484 GGGTGACTCTTTTCTAAAGGTGGTGGGAGTATCTGTCGGGGTGGTGTGGCCCTTGGATGG 2543
              |||| | |||||||||||||||||| || | || | | ||||||||          ||| |
Db       5328 GGGTAATTCTTTTCTAAAGGTGGTAGGGG-ATTTCTGGGGGTGGTCCA-------GATTG 5277

Qy       2544 GTCAGGTGGGTGTGAGAGGTCCTGGGGAGGTGGGCGTT-GAGCTCAAAGTTGTCCTACTG 2602
              |||| || ||||   ||||| |||||| | ||||  | ||    | |||||||| || ||
Db       5276 GTCAAATGTGTGTAGCAGGTCATGGGGAAGGGGGCCATGGAAACCCAAGTTGTCATAATG 5217

Qy       2603 CCATGTTTTTGTACCTGAAATAAAGCATATTTTGCACTTGTTACTGTACCATAGTGCGGA 2662
              |||||||||||||||||||||||||||||||||||||||| |                 |
Db       5216 CCATGTTTTTGTACCTGAAATAAAGCATATTTTGCACTTGTAA----------------A 5173

Qy       2663 CGAGAAGTCTGTATGTGGGATCTGTGCTTGGGTTAGAATGCAAATAAAAC 2712
              |||||  |||||||||||| |||||||  |||||  ||||||||||||||
Db       5172 TGAGAAATCTGTATGTGGGCTCTGTGC-TGGGTCAGAATGCAAATAAAAC 5124


RESULT 14
AC136817
LOCUS       AC136817               231580 bp    DNA     linear   HTG 23-NOV-2002
DEFINITION  Rattus norvegicus clone CH230-43B4, *** SEQUENCING IN PROGRESS ***,
            2 unordered pieces.
ACCESSION   AC136817
VERSION     AC136817.2  GI:25188334
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.

REFERENCE   1  (bases 1 to 231580)
  AUTHORS   Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
            Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
            Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
            Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
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            Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
            Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
            Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
            Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
            Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
            Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
            Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
            Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
            Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
            Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
            Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
            Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
            Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
            Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M.,
            Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A.,
            Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
            Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
            Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
            Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
            Lorensuhewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J.,
            Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A.,
            Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
            Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,
            Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S.,
            Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L.,
            Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
            Nwaokelemeh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K.,
            Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C.,
            Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L.,
            Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,
            Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
            Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,
            Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,
            Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D.,
            Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,
            Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C.,
            Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K.,
            Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J.,
            Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
            Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K.,
            Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
            Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
            Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
            Weinstock,G. and Gibbs,R.A.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 231580)
  AUTHORS   Rat Genome Sequencing Consortium.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-NOV-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
REFERENCE   3  (bases 1 to 231580)
  AUTHORS   Rat Genome Sequencing Consortium.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-NOV-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     On Nov 23, 2002 this sequence version replaced gi:24796690.
            The sequence in this assembly is a combination of BAC based reads
            and whole genome shotgun sequencing reads assembled using Atlas
            (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
            in the feature table below represents a scaffold in the Atlas
            assembly (a 'contig-scaffold'). Within each contig-scaffold,
            individual sequence contigs are ordered and oriented, and separated
            by sized gaps filled with Ns to the estimated size. The sequence
            may extend beyond the ends of the clone and there may be sequence
```

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            contigs within a contig-scaffold that consist entirely of whole
            genome shotgun sequence reads. Both end sequences and whole genome
            shotgun sequence only contigs will be indicated in the feature
            table.
            -------------- Genome Center
                Center: Baylor College of Medicine
                Center code: BCM
                Web site: http://www.hgsc.bcm.tmc.edu/
                Contact: hgsc-help@bcm.tmc.edu
            -------------- Project Information
                Center project name: KCLR
                Center clone name: CH230-43B4
            -------------- Summary Statistics
                Assembly program: Phrap; version 0.990329
                Consensus quality: 204259 bases at least Q40
                Consensus quality: 209008 bases at least Q30
                Consensus quality: 211699 bases at least Q20
                Estimated insert size: 211394; sum-of-contigs estimation
                Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
            --------------
            * NOTE: Estimated insert size may differ from sequence length
            *   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 2 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *       1   230160: contig of 230160 bp in length
            *  230161   230260: gap of unknown length
            *  230261   231580: contig of 1320 bp in length.
FEATURES             Location/Qualifiers
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                     /organism="Rattus norvegicus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10116"
                     /clone="CH230-43B4"
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                     /note="wgs_end_extension
                     clone_end:Sp6"
     misc_feature    1338. .2663
                     /note="wgs_end_extension
                     clone_end:Sp6"
     misc_feature    9136. .9761
                     /note="clone_boundary
                     clone_end:Sp6
                     site:EcoRI
                     end_sequence:BH263051"
     misc_feature    43876. .45375
                     /note="wgs_contig"
     misc_feature    complement(225032. .225921)
                     /note="clone_boundary
                     clone_end:T7
                     site:EcoRI
                     end_sequence:BH263050"
     misc_feature    229121. .230160
                     /note="wgs_end_extension
                     clone_end:T7"
ORIGIN

  Query Match             3.2%;  Score 87.6;  DB 2;  Length 231580;
  Best Local Similarity   65.6%;  Pred. No. 2.9e-10;
  Matches  269;  Conservative    0;  Mismatches   99;  Indels   42;  Gaps    8;

Qy       2304 CTGCTGGGAAAAGCTTTGCGGGGCTTGCTTGGTTAACCACAGAAGAGAAGGGGACTGTTT 2363
             ||||||||  | |||||  | |||||      | ||      | | |||  |||| |||||||||
Db     225296 CTGCTGGGGAGAGCTTAGTGGGGC-----TAGTATCAGAGACAAGCAAAGGAGACTGTTT 225350

Qy       2364 GGGGTGCCTCTCTGCAGCCTCCCCGTGCTGGGTGGAAGCACGGTTACTGTGTTCTCTAAT 2423
                |   | ||       |||  | ||||||||  | ||  |||||||||||||| | ||
Db     225351 CATG---CACTGACTTATCTCTTCCTGCTGGGTAAAGGCTTGGTTACTGTGTTCTTTCAT 225407

Qy       2424 GTTCATGTATTTAAAATGATTTCTTTCTAAAGATGTAACCTCCACACCTTTCTCCAGATT 2483
             ||       |       |||  | ||    | |         |     |  ||| ||| || |
Db     225408 GCTTCGAAGTGATTCCTGAGGTTTTCTCACA--------CCTACCTTCTTCCTCTAGGTG 225459

Qy       2484 GGGTGACTCTTTTCTAAAGGTGGTGGGAGTATCTGTCGGGGTGGTGTGGCCCTTGGATGG 2543
             |||| | ||||||||||||||||| || | || | | ||||||||        ||| |
Db     225460 GGGTAATTCTTTTCTAAAGGTGGTAGGGG-ATTTCTGGGGGTGGTCCA-------GATTG 225511

Qy       2544 GTCAGGTGGGTGTGAGAGGTCCTGGGGAGGTGGGCGTT-GAGCTCAAAGTTGTCCTACTG 2602
             ||||  || ||||   ||||| |||||| | ||||  | ||   | |||||||| || ||
Db     225512 GTCAAATGTGTGTAGCAGGTCATGGGGAAGGGGGCCATGGAAACCCAAGTTGTCATAATG 225571

Qy       2603 CCATGTTTTTGTACCTGAAATAAAGCATATTTTGCACTTGTTACTGTACCATAGTGCGGA 2662
             ||||||||||||||||||||||||||||||||||||||||| |                |
Db     225572 CCATGTTTTTGTACCTGAAATAAAGCATATTTTGCACTTGTAA----------------A 225615

Qy       2663 CGAGAAGTCTGTATGTGGGATCTGTGCTTGGGTTAGAATGCAAATAAAAC 2712
              ||||| ||||||||||| |||||||  |||| ||||||||||||||||
Db     225616 TGAGAAATCTGTATGTGGGCTCTGTGC-TGGGTCAGAATGCAAATAAAAC 225664


RESULT 15
CNS01DT7
LOCUS       CNS01DT7              182643 bp    DNA     linear   PRI 14-MAY-2001
DEFINITION  Human chromosome 14 DNA sequence BAC R-131H24 of library RPCI-11
            from chromosome 14 of Homo sapiens (Human), complete sequence.
ACCESSION   AL132642
VERSION     AL132642.4  GI:14041778
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 182643)
  AUTHORS   Heilig,R., Petit,J.L., Vico,V., Dasilva,C., Robert,C., Wincker,P.,
            Brottier,P., Cattolico,L., Barbe,V., Pelletier,E., Artiguenave,F.,
            Levy,M., Eckenberg,R., Bruls,T., deBerardinis,V., Cruaud,C.,
            Gyapay,G., Saurin,W. and Weissenbach,J.
  TITLE     Sequencing of the human chromosome 14
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 182643)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-MAY-2001) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     On May 15, 2001 this sequence version replaced gi:8217878.
            -------------- Genome Center
            Center: Genoscope / Centre National de Sequencage
            Center code: GS
            Web site: http://www.genoscope.cns.fr/
            Contact: SeqRef@genoscope.cns.fr
            --------------
            The following BAC sequence is oriented from the T7 to the SP6 end.
            Upstream BAC (overlapping the T7 end) : R-187A6
            Downstream BAC (overlapping the SP6 end) : R-1089B7 (AC=AL079302)
            -------------- Summary Statistics
            Assembly program: Phrap; version 2.0
            Quality coverage: 7.83x in Q20 bases; sum-of-contigs
            --------------
            ------------------------
            Overall quality chart :
            Range     :   bases
            0         :
            1  -  9   :
            10 - 19   :
            20 - 29   :      11
            30 - 39   :      83
            40 - 49   :    1023
            50 - 59   :    1882
            60 - 69   :    4058
            70 - 79   :   15227
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            80 - 89  :   59044
            90 - 99  :  101315
            ----------------------
            Percentage of bases with a quality value >= 40 : 99 %.
FEATURES             Location/Qualifiers
     source          1. .182643
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="14"
                     /clone="R-131H24"
                     /clone_lib="RPCI-11"
     STS             138601. .138720
                     /note="matching EMBL:AA421158
                     RHdb:RH93218
                     dbSTS:STS66221
                     Identified using the e-PCR software (G. Schuler)"
     STS             157690. .157856
                     /note="matching EMBL:T03336
                     RHdb:RH53909
                     dbSTS:STS10403
                     Identified using the e-PCR software (G. Schuler)"
     STS             162845. .162997
                     /note="matching EMBL:AA610019
                     RHdb:RH94166
                     dbSTS:STS67159
                     Identified using the e-PCR software (G. Schuler)"
     STS             167731. .167886
                     /note="matching EMBL:AA195225
                     RHdb:RH65774
                     dbSTS:STS45705
                     Identified using the e-PCR software (G. Schuler)"
ORIGIN

  Query Match             2.9%;  Score 81;  DB 9;  Length 182643;
  Best Local Similarity   54.5%;  Pred. No. 1.3e-08;
  Matches  213;  Conservative    0;  Mismatches  165;  Indels   13;  Gaps    2;

Qy        940 GCTGTTTATGCCACTGATTTATGATAGGGAATATTATCTTTGAACCCAATGAAGTGTTTT 999
              | ||  ||| |    || || ||||| | ||| |||||||||| ||||  |    ||
Db      36767 GATGAATATTCTTTTGTTTGATGATGGAGAACATTATCTTTAAACCACAATTAGGCAAAA 36826

Qy       1000 CTCCCCCATCACAAAAAAAAAAATTCTTATTTTTAGTAGACATGTATTTACCAAAAATAT 1059
                |   |     ||||| ||       || | |        | |  ||| ||  ||||   |
Db      36827 TGCTATCCCATAAAAAAGAATTCCATTTTTCTCATTAGTAGACCTATATAATAAAATATT 36886

Qy       1060 GTACTCAATTATTGTATTTTGGATTTTATCAATTTAAAAATTGTGGAAATTTGTTTGCTC 1119
              ||||| | ||||| | ||||  |||| ||||| | | || || ||||||||||||   ||
Db      36887 GTACTTAGTTATTATGTTTTAAATTTCATCAA-TAATAATTTATGGAAATTTGTTCTGTC 36945

Qy       1120 TTA------------CGCCAACATAATATTGATTTTGCCTCTTGGCTCTGAAAGCCCAAA 1167
              ||            |  ||  |||  |||||| ||||||||||    | |||| |||
Db      36946 TTGTTATGTAAGTGTCTGCATAATATCCTTGATTCTGCCTCTTGGCCTGCACAGCCTAAA 37005

Qy       1168 ATATTTACCGTCTAGCCCGTTACAGAAAAAGTCTGCTGACTACTGAGCCAGACCTCCATT 1227
              ||| ||||  ||| | ||  | ||||| |||| |||||||| |||  |
Db      37006 ATACTTACTATCTGGTCCTCTGCAGAACAAGTATGCTGACTCCTGCTCTTTTTGATGGGA 37065

Qy       1228 ACCTCCATCCCTGTTGGATTATTTAAAGAAAGCCTCAGACAGTAAGGGCTTTTTTAAAAG 1287
                | ||||  ||      |  | | |||  |       |  || ||       | |||| ||
Db      37066 TATTTCATCTTTGAATTTTGTTCTCAAGCCAAGAAATGGAAGGAATCAGACTGTTAAGAG 37125

Qy       1288 AATAAAATGACTTGGTTTGCGCTTGGAAGCA 1318
                ||| | | | |    |   |   || ||
Db      37126 CTGGAAAGGCCCTCGGAGGTCTTCTAAACCA 37156


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Job time : 11599 secs
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